

AA051543;
 XX XX
 DT 25-MAR-2003 (updated)
 DT 24-MAY-1994 (first entry)
 XX XX
 DE Lipopolysaccharide induced protein gene.
 XX XX
 KM Macrophage; induced; lipo-polysaccharide; antitumour;
 KM antiinflammatory; trypanocidal agent; antibody; cell proliferation;
 KM activation; cytotoxicity; ds.
 XX XX
 OS Homo sapiens.
 XX XX
 FH Key Location/Qualifiers
 FT CDS 1810..3315
 FT /tag= a
 FT 1980..2228
 FT /tag= b
 FT /note= "Intron 1 is only partially sequenced
 (represented by (N)40 in the sequence
 estimated length ca. 5400 bp"
 FT intron 2615..2846
 FT /tag= c
 FT /note= "Intron 2 is only partially sequenced
 (represented by (N)40 in the sequence
 estimated length ca. 7900 bp"
 FT intron 2907..2995
 FT /tag= d
 FT /note= "Intron 3 is only partially sequenced
 (represented by (N)40 in the sequence
 estimated length ca. 1000 bp"
 FT polyA_signal 3841..3846
 FT /tag= e
 XX XX
 PN WO9322437-A1.
 XX XX
 PD 11-NOV-1993.
 XX XX
 PF 28-APR-1993; 93WO-EP01022.
 XX XX
 PR 30-APR-1992; 92EP-0401231.
 XX XX
 PA (INNO-) INNOGENETICS NV SA.
 XX XX
 PI Devos K, Franssen L, Van De Voorde A, Van Heuvels W H.
 X
 WPI, 1993-368796/46.
 -R P-PSDB; AAR43682.
 XX XX
 PT New polypeptide induced in macrophage(s) by lipo-polysaccharide -
 PT useful e.g. as antitumour, antiinflammatory or trypanocidal
 PT agent, also related nucleic acid, antibodies, anti-sense cpds.
 PT etc.
 XX XX
 PS Claim 9; Fig 1; 108bp; English.
 XX XX
 CC The polypeptide induced in macrophages by lipopolysaccharide
 CC stimulates cell proliferation (esp. when costimulated with IL-4)
 CC promote activation, cytotoxicity, and mobilisation of LAK cells;
 CC promote recruitment of suppressive peritoneal exudate cells;
 CC promote generation of immunocompetent lymph node cells (LNC) and
 CC have trypanocidal and trypanolytic activity. The human and murine
 CC sequences are given in (AA051543-45), peptide fragments able to
 CC generate antibodies are given in (AAR51951-61)
 CC (updated on 25-MAR-2003 to correct PN field.)
 CC XX
 SQ Sequence 3861 BP; 542 A; 1241 C; 1292 G; 658 T; 128 other;
 Query Match 15.1%; Score 69.2; DB 14; Length 3861;
 Best Local Similarity 53.1%; Pred. No. 0.0015;
 Matches 170; Conservative 0; Mismatches 148; Indels 2; Gaps 1;
 35 CAGCCCTGGCTGGCGAAGGCGGAGGCGCCGCTCGGTGGAGACTGGGGGTG 94

Db 2086 CTGCCCCGCGCCGCCCCCGGCGCCCGCACGCTCGGCGGCGCGGAGCGG 2027
 QY 95 GAGGTGCCCGAGACCTACCCAGCGCGGAGTACTCCGCTCAACACTCGGAGCTGCA 154
 Db 2026 GACGCGAAGGAGGAGGCGCGGCGCGGAGTCTCGCGCCACACTACCTCCCTTCAGC 1967
 QY 155 TCCCTGGGTGGCCCGCGAGACGCTGCGCGGCGTGAAGAGATGCGGAGCGGAGCGGAG 214
 Db 1966 TGCACCGGTGCTGAGATGATGCGCGCCCGCGCCCGACAGCCCGGCGAGAGACAGA 1907
 QY 215 GCGGGGCGGCGCTTCGTCACGTGAGAGAGCGCGCGGCGCGGCGCGGCGCGCGCG 274
 Db 1906 GCAGCAGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1847
 QY 275 CCGGCTCTTAAAGCGCGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 334
 Db 1846 CCG 1789
 QY 335 GCCCGGCGGAGACGCGGAGAC 354
 Db 1788 CCGGCGCGCGCGCTCGCGAGC 1769
 RESULT 14
 ID AAX53491 standard; DNA; 114955 BP.
 AC AAX53491;
 XX XX
 DT 05-JUL-1999 (first entry)
 XX XX
 DE Human adenosine A1 receptor antisense oligonucleotide fragment.
 XX XX
 KW Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.
 XX XX
 OS Synthetic.
 XX XX
 PN WO9213886-A1.
 XX XX
 PD 25-MAR-1999.
 XX XX
 PF 17-SEP-1998; 98WO-US19419.
 XX XX
 PR 09-JUN-1998; 98US-0093972.
 XX XX
 PR 17-SEP-1997; 97US-0059160.
 XX XX
 PA (UWEC-) UNIV EAST CAROLINA.
 XX XX
 PI Nyce JW;
 XX XX
 DR WPI, 1999-229400/19.
 XX XX
 CC New antisense oligonucleotides used in treatment of, e.g. pulmonary
 CC vasoconstriction
 PT
 PS Disclosure: Page 37; 120bp; English.
 XX XX
 CC The specification describes antisense oligonucleotides (AAX52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one

DE Human neuronal NACHR alpha7 subunit encoding cDNA.
 XX
 XX Human; neuronal; nicotinic acetylcholine receptor; NACHR; drug screening;
 KW Immunochimetry; NACHR alpha7 subunit; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 73..1581
 FT /tag= a
 FT /product= "NACHR alpha7 subunit"
 FT /note= "neuronal nicotinic acetylcholine receptor"
 XX
 PN WO200259266-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 29-OCT-2001; 2001MO-US50985.
 XX
 PR 01-NOV-2000; 2000US-0703951.
 XX
 TA (MERI) MERCK & CO INC.
 XI Gillespie A, Claeps BO, Chavez-Noriega LE, Siegel R, Elliott KJ;
 XX WPI; 2002-698532/75.
 DR P-PSDB; AB882435.
 XX
 PT Cell comprising nucleic acids encoding human alpha and beta subunits of
 PT neuronal nicotinic acetylcholine receptors, useful for in vitro
 PT screening of a drug substance in a test system specific for humans
 XX
 PS Examples: Page 129-130; 143pp; English.
 XX
 CC The invention relates to a suitable host cell transfected with an
 CC isolated nucleic acid molecule comprising a sequence of nucleotides or
 CC ribonucleotides that encodes at least one alpha or beta subunit of a
 CC human neuronal nicotinic acetylcholine receptor (NACHR). The compositions
 CC and methods of the present invention, which provide a means to prepare
 CC synthetic or recombinant receptors and receptor subunits that are
 CC substantially free of contamination from many other receptor proteins,
 CC are useful for observing the effect of a drug substance on a particular
 CC subtype to perform in vitro screening of the drug substance in a test
 CC system that is specific for humans. The antibodies can be used in
 CC immunochemistry and for diagnostic and therapeutic applications. The
 CC present sequence represents a human neuronal NACHR alpha7 subunit
 CC encoding cDNA.
 XX
 SQ Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 1 other;
 XX
 Query Match 27.8%; Score 127; DB 24; Length 1876;
 Best Local Similarity 100.0%; Pred. No. 3.8e-13;
 Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 321 GGGCGAGGCGGAGCGCGGCGAGACGTCGAGCGCGGCTGCTGCAGCT 380
 DB 1 GGGCGAGGCGGAGCGCGGCGAGACGTCGAGCGCGGCTGCTGCAGCT 60
 QY 381 CCGGAGCTCAACATGCGCTGCTGCGGAGGCGTCTGCGCTGCGCTGCTGCTC 440
 DB 61 CCGGAGCTCAACATGCGCTGCTGCGGAGGCGTCTGCGCTGCGCTGCGCTC 120
 QY 441 CTGCACG 447
 DB 121 CTGCACG 127

RESULT 12
 ID ABS54875
 XX ABS54875 standard; cDNA; 1876 BP.
 AC
 XX ABS54875;

DT 06-DEC-2002 (first entry)
 XX
 XX Human neuronal nicotinic acetylcholine receptor alpha 7 subunit cDNA.
 DE
 XX Human; neuronal; nicotinic acetylcholine receptor; nNACHR; gene; ss;
 KW ion flux; alpha 7 subunit.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 73..1581
 FT /tag= a
 FT /product= "Human nNACHR alpha 7 subunit"
 XX
 PN US6440681-B1.
 XX
 PD 27-AUG-2002.
 XX
 PF 07-JUN-1995; 95US-0487596.
 XX
 PR 03-APR-1990; 90US-0504455.
 XX
 PR 30-NOV-1992; 92US-0938154.
 PR 08-MAR-1993; 93US-0028031.
 PR 08-NOV-1993; 93US-0149503.
 XX
 TA (MERI) MERCK & CO INC.
 XX
 PI Elliott KJ, Ellis SB, Harpold NM;
 XX WPI; 2002-711528/77.
 DR P-PSDB; AB670492.
 XX
 PT Identifying antagonists or agonists of human neuronal nicotinic
 PT acetylcholine receptors, by contacting recombinant cells with test
 PT compound, and measuring ion flux of cells or binding of compound to
 PT nNACHR
 XX
 PS Claim 101; Column 57-60; 56pp; English.
 XX
 CC The invention relates to a method for identifying compounds that are
 CC antagonists or agonists of human neuronal nicotinic acetylcholine
 CC receptors (nNACHRs), by contacting recombinant cells with a test
 CC compound and measuring ion flux, the electrophysiological response of the
 CC cells or binding of the test compound to the nNACHR. The recombinant
 CC cells are produced by transfection with a nucleic acid encoding at least
 CC one human nNACHR (alpha or beta) subunit, such that the cells express an
 CC nNACHR comprising one human subunit encoded by the transfected nucleic
 CC acid. This sequence represents cDNA encoding the alpha 7 subunit of the
 CC human nNACHR polypeptide.
 XX
 SQ Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 1 other;
 XX
 Query Match 27.8%; Score 127; DB 24; Length 1876;
 Best Local Similarity 100.0%; Pred. No. 3.8e-13;
 Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 321 GGGCGAGGCGGAGCGCGGCGAGACGTCGAGCGCGGCTGCTGCAGCT 380
 DB 1 GGGCGAGGCGGAGCGCGGCGAGACGTCGAGCGCGGCTGCTGCAGCT 60
 QY 381 CCGGAGCTCAACATGCGCTGCTGCGGAGGCGTCTGCGCTGCGCTGCTGCTC 440
 DB 61 CCGGAGCTCAACATGCGCTGCTGCGGAGGCGTCTGCGCTGCGCTGCGCTC 120
 QY 441 CTGCACG 447
 DB 121 CTGCACG 127

RESULT 13
 ID AAQ51543/c
 XX AAQ51543 standard; DNA; 3861 BP.
 AC
 XX

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XX 14-MAY-1998 (first entry)
DT
XX
DE Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA.
XX
XX Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
KW brain tissue; screening; NACnR; antibody; ds.
XX
XX Homo sapiens.
OS
XX
XX Location/Qualifiers
FH Key 73..1581
FT CDS /tag= a
FT /product= "neuronal nicotinic acetylcholine receptor
FT alpha-7 subunit"
XX
XX WO9420617-A2.
XX
XX 15-SEP-1994.
XX
XX 08-MAR-1994; 94WO-US02447.
XX
XX 08-MAR-1993; 93US-0028031.
XX
XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX
XX Eliott KJ, Ellis SB, Harpold MM;
XX
XX WPI; 1994-303024/37.
XX P-PSDB; AAM44153.
XX
XX Human neuronal nicotinic acetylcholine receptor subunits and DNA -
XX also transformed cells useful for screening cpds. which modulate
XX activity of the receptor
XX
XX Claim 8; Page 78-79; 99pp; English.
XX
XX The present sequence encodes a human neuronal nicotinic acetylcholine
XX receptor (NACnR) subunit. The cells expressing the alpha and/or beta
XX NACnR subunits may be used in a method of screening compounds to
XX identify any which modulate the activity of human neuronal NACnR.
XX Subunit specific antibodies may be used to monitor the distribution
XX and expression density of various subunits in normal vs diseased brain
XX tissues. Testing of single receptor subunits or specific receptor
XX subunit combinations with a variety of potential agonists or antagonists
XX provides information with respect to the function and activity of the
XX individual subunits and should lead to the identification and design of
XX compounds that are capable of very specific interaction with one or
XX more receptor subtypes. The resulting drugs should exhibit fewer
XX unwanted side effects than drugs identified e.g. screening with cells
XX that express a variety of subtypes.
XX
XX Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 1 other;
SQ
Query Match 27.8%; Score 127; DB 15; Length 1876;
Best Local Similarity 100.0%; Pred. No. 3.8e-13;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 321 GGGCGGAGGCGGAGCGCGGCGGAGAGCGTGAAGCGCGGCTGCTGAGCT 380
DB 1 GGGCGGAGGCGGAGCGCGGCGGAGAGCGTGAAGCGCGGCTGCTGAGCT 60
QY 381 CCGGAGCTCAACATGCGCTGCTGCGCGGAGGCGTGTGCGTGGCGCGTGCCTC 440
DB 61 CCGGAGCTCAACATGCGCTGCTGCGCGGAGGCGTGTGCGTGGCGCGTGCCTC 120
QY 441 CTGCACG 447
DB 121 CTGCACG 127
RESULT 10
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AAT48239
ID AAT48239 standard; DNA; 1876 BP.
XX
XX AAT48239;
XX
XX 09-APR-1997 (first entry)
DT
XX
XX Neuronal nicotinic acetylcholine receptor alpha-7 subunit DNA.
DE
XX
XX Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
KW ligand-gated receptor; ds.
XX
XX Homo sapiens.
OS
XX
XX Location/Qualifiers
FH Key 73..1581
FT CDS /tag= a
FT /product= a
XX
XX WO9641876-A1.
XX
XX 27-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US09775.
XX
XX 07-JUN-1995; 95US-0484722.
XX
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX
XX Eliott KJ, Harpold MM;
XX
XX WPI; 1997-065463/06.
XX P-PSDB; AAM09025.
XX
XX Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
XX used in screening to determine the effect of drugs on the receptor
XX
XX Disclosure; Page 71-73; 108pp; English.
XX
XX A DNA sequence (AAT48239) codes for the alpha-7 subunit (AAM09025) of
XX the human neuronal nicotinic acetylcholine receptor (NACnR). Host
XX cells, esp. mammalian cells or amphibian oocytes, carrying alpha-7
XX nucleic acids, opt. in combination with other alpha and/or beta
XX subunit nucleic acids (see also AAT48232-38, AAT48240-41), express
XX recombinant NACnR subunits useful for identifying cpds. that
XX modulate the activity of human NACnRs.
XX
XX Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 other;
SQ
Query Match 27.8%; Score 127; DB 18; Length 1876;
Best Local Similarity 100.0%; Pred. No. 3.8e-13;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 321 GGGCGGAGGCGGAGCGCGGCGGAGAGCGTGAAGCGCGGCTGCTGAGCT 380
DB 1 GGGCGGAGGCGGAGCGCGGCGGAGAGCGTGAAGCGCGGCTGCTGAGCT 60
QY 381 CCGGAGCTCAACATGCGCTGCTGCGCGGAGGCGTGTGCGTGGCGCGTGCCTC 440
DB 61 CCGGAGCTCAACATGCGCTGCTGCGCGGAGGCGTGTGCGTGGCGCGTGCCTC 120
QY 441 CTGCACG 447
DB 121 CTGCACG 127
RESULT 11
ABV73248
ID ABV73248 standard; cDNA; 1876 BP.
XX
XX ABV73248;
XX
XX 22-JAN-2003 (first entry)
XX
```

CC ABD13410-ABQ5121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.

Sequence 556 BP; 66 A; 71 C; 192 G; 227 T; 0 other;

| | | | | |
|-----------------------|--------------|-------------------|----------------|------------|
| Query Match | 46.5% | Score 212.4 | DB 24 | Length 556 |
| Best Local Similarity | 68.4% | Pred. No. 2.5e-27 | | |
| Matches 294 | Conservative | 0 | Mismatches 136 | Indels 0 |
| | | | Gaps | 0 |

| | | | |
|----|-----|--|-----|
| QY | 28 | CCCTGGGCGAGCCCTTGCTGGCCAGAGGCGCGAGGCGCGAGGCCGCTCGGTGAGACT | 87 |
| Dp | 554 | CCCTTAACGAACCCCTTAACCTTAACGAAAAACCGGAAACCGGAAACCCGCTCGATTAATAACT | 495 |
| QY | 88 | GGGGGTGGAGGTGCTCCGAGCGTACCAGCGCGGAGTACTCTCCGCTCAACACTCGGG | 147 |
| Dp | 494 | AAAAATAAAAAATACCGGAAACGTATCCCAACGCCGAAAAATACCTCCGCTCAACACTGGAA | 435 |
| QY | 148 | CTGCATTCCTCGGGTGGGCGCGCGCGAGCGCTGCGCCCGGCGTGGAGGATGGCGGGGGGG | 207 |
| Dp | 434 | CTACATTCCTCTAAATATACCGCGGAAACGCTTAACCGGAACTTAATAAAAAATAAAAAAGAA | 375 |
| / | 208 | GACGGGGGCGGGGCGGGGCTGTCACGTGAGAGCGCGCGGGGCGGGCGGGCGGGG | 267 |
| Dp | 374 | AACGAAAAAGAAACGAAACCTGTCACGTAAAAAATACCGCGGAAACGAAACGAAACGAAA | 315 |
| QY | 268 | GGCGCGCGCCGCGCTCTTTAAGCGCGCGAGCCGAGCGGAGTGGCTCTTGCGCGCA | 327 |
| Dp | 314 | ACGCGCGCCGACTCTCTTAAAAACCGCGGAAACCGAACGACAAATTAACCTTAATAACGCA | 255 |
| QY | 328 | GGCGGAGCGCGCGGCGAGCGAGTGAAGCGCGCGCGGCTGCTGCTCACTCCGGAC | 387 |
| Dp | 254 | AACGCAAAACCGAAACGACAAACGAAACGTAAACCGCGGACTGCTACAACTCGAAAC | 195 |
| QY | 388 | TCAACATGCGTCTTCGCCGGAGGCGTGTGGCTGGCTGGCGCGCTGCTCTTCGACG | 447 |
| Dp | 194 | TCAACATAGCTACTCGCGGAAAAAGTCTTAACGTAAACGCTAACCGCGTGGCTCTTAACG | 135 |
| QY | 448 | GTTAAAGCCAC | 457 |
| Dp | 134 | ATPAAACCAAC | 125 |

RESULT 8
ABQ47035
ID ABQ47035 standard; DNA; 556 BP.
...

| | |
|----|---------------------------|
| AC | ABQ47035; |
| XX | |
| nn | 12-JUL-2002 (first entry) |

Oligonucleotide for detecting cytosine methylation SEQ ID NO 33626.

KW Human cytosine methylation; 5'-ppg-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism
 KW SNP; cell differentiation; ds.

Homo sapiens.

WO200218632-A2.

07-MAR-2002.

01-SEP-2001; 2001WO-EP10074.

01-SEP-2000; 2000DE-1043826.

(EDIC-) PRICENOWTOS 20

Chapman, D. 1997. *Dispersal Ecology*. Blackwell Science, Oxford.

DR WPI; 2002-371829/40.

PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis; comprises selective hybridization of
PT amplicons from chemically treated DNA -

PS Claim 12; 56pp + Sequence Listing; 56pp; German

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. AB01310-AB054121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.

SQ Sequence 556 BP; 227 A; 192 C; 71 G; 66 T; 0 other;

| | | | | |
|-----------------------|--------------|-------------------|----------------|------------|
| Query Match | 46.5% | Score 212.4 | DB 24 | Length 556 |
| Best Local Similarity | 68.4% | Pred. No. 2.5e-27 | | |
| Matches 294 | Conservative | 0 | Mismatches 136 | Indels 0 |
| | | | | Gaps 0 |

| | | | |
|----|-----|--|-----|
| QY | 28 | CCCTGGGCAAGCCCTGAGCCTGGCCAGAGGCGCGAGGCCGAGAGCCGCTGGTGGAGACT | 87 |
| Db | 3 | CCTTTAAACAACCCCTTAACCTTAACCAAAAAACGAAACCGAAACCCGCTGCATTAATAACT | 62 |
| QY | 88 | GGGGGTGAGAGTGCCCGGAGCGTACCAGCGCCGGAGTACTCTCCGCTCAACCTCGGG | 147 |
| Db | 63 | AAAAATAAAATAATACCGAAAGCTAACCCAAACGCCGAAAAATACCTCCCGCTCACACTCGAA | 122 |
| QY | 148 | CTGCATTTCCCTGGGTGGTGGGCGCCCGCAGAGCTTGCGCTCGCGGCTTGAGGGATGGCGGGCGGG | 207 |
| Db | 123 | CTTCAATTTCCCTAAATAACCGCGCGAAAGCTTAACCCGAACTTAAAAATAAAAAAGAA | 182 |
| QY | 208 | GACGGGGGCGGGGCGGGGCTGCTACGTTGAGAGAGCGCGGGGCGCGGCGGGGCGGGG | 267 |
| Db | 183 | AACGAAAAAGAAAAAGAAACTGCTACCTTAAAAAAAACGCGGAAAAAGAACGAAACGAAA | 242 |
| QY | 268 | GCGCGCGCCCGCTCCTTAAAGCGCGCGAGCCGAGCGCGAGGTGCTCTGTGGCCGCA | 327 |
| Db | 243 | ACCGCGGCCCGCACTCCTTAAAAACCGCGGAAACCGAACGACGAAATACCTTATTAACGCA | 302 |
| QY | 328 | GGGGCAGGCGCGGGGGAACGCGAGAGCGTGAAGGCGCGCGGCTGCTGCAGCTCCGGGAC | 387 |
| Db | 303 | AACGCAAAACCGAACGACACGAAACGTTAAAGCGCGCGACTGCTACCACTCCGAAC | 362 |
| QY | 388 | TCAACAATGGCTGCTCGCGCGGAGGCGTCTGAGCTTGCTGGCCGCTGCTCTGCACG | 447 |
| Db | 363 | TCAACATACGTAATCGCGGAAAAACGTTAACTTAACGCTTAACCGCGTGGCTCTACAG | 422 |
| QY | 448 | GTTAAAGCAC 457 | |
| Db | 423 | ATTAACACAC 432 | |

| | |
|-------------|-------------------------|
| RESULT 9 | |
| AAV12197 | |
| ID AAV12197 | standard; cDNA; 1876 BP |

AC AAV12197

| ID | ABL34019 standard, DNA; 5304 BP. |
|---|---|
| ABL34019/C | |
| ABL34019 | |
| 26-MAR-2002 | (first entry) |
| Human immune system associated gene SEQ ID NO: 1992. | |
| Human; immune system disease; cytosine methylation; antiaesthetic; antiadrenergic; antianemic; cytoseric; noctropic; neuroprotective; anti-HIV; anticomulant; ophthalmological; antihumoral; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene; ds. | |
| OS Homo sapiens. | |
| PN WO200200928-A2. | |
| XX | |
| PD 03-JAN-2002. | |
| XX | |
| PF 02-JUL-2001; 2001WO-EP07537. | |
| XX | |
| PR 30-JUN-2000; 2000DE-1032529. | |
| XX | |
| PR 01-SEP-2000; 2000DE-1043826. | |
| XX | |
| PA (EPIG-) EPIGENOMICS AG. | |
| XX | |
| PI Olek A, Piepenbrock C, Berlin K; | |
| XX | |
| PI WPI; 2002-130909/17. | |
| XX | |
| PT Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation - | |
| XX | |
| PS Claim 1; SEQ ID NO 1992; 32pp + Sequence Listing; German. | |
| XX | |
| CC The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention. | |
| XX | |
| XX | |
| SO Sequence 5304 BP; 1400 A; 152 C; 1205 G; 2547 T; 0 other; | |
| Query Match | 49.5%; Score 221.8; DB 24; Length 5304; |
| Best Local Similarity | 67.8%; Pred. No. 4.7e-29; |
| Matches 310; Conservative 0; Mismatches 147; Indels 0; Gaps 0; | |
| QY 1 AGAAGCGAAGGAGGAGTGAAGAGCTGGGCTTGGGAGGCGCTGGCTGGCCAGAGGCGCG 60 | |
| DB 696 AAAACGCAAAAATAAATAAATTAACCTTAACCTTAACCAACCTTAACCTTAACCAAAAACGCG 637 | |
| QY 61 AGGCGGAGAGCGCGCTCGGTGAGACTGGGGGTGAGAGTGGCCGAGAGCGTACCGAGCGCC 120 | |
| DB 636 AAACCGAAGAACCGCGGTGATTAATAAATAAATAAATAAATTAACCGAAGAGTACCAAGCC 577 | |
| QY 121 GGAAGTACTCTCCGCTCAACACTTGGGCTGCAATTCCCTGGGTGGCCCGGAGACGCTGG 180 | |
| DB 576 GAAATATCTCTCCGCTCAACACTTGGGCTGCAATTCCCTTAATAATAACCGCGAAGCGTAA 517 | |
| QY 181 CCGGAGCTGAGGAGGATGGCGGGGCGGGGAGCGGGGCGGGGCGTCTGCAAGTGGAG 240 | |
| DB 516 CCGGAGCTGAGGAGGATGGCGGGGCGGGGAGCGGGGCGGGGCGTCTGCAAGTGGAG 457 | |

| | | | |
|----------|---|--|------|
| QY | 241 | AGGCGCGCGGGGCGGCGGGGCGGCGCGCGCGCTCCTTAAAGCGCGCAGCC | 30 |
| Db | 456 | AAACCGCGGAAAAACGAAACGAAACGCGCGCCGACTCTTAAAAACGCGCAAC | 3577 |
| QY | 301 | GAGCGCGAGGTGCTCTTGTGGCGCGCAGCGCGAGGCCCGGAGCAGCGAGCGTGGAG | 3608 |
| Db | 396 | GAAAGACGAAATACCTCTTATTAACCGCAAAACCGAAGACGACAGCAACGAAACGTAAAA | 3377 |
| QY | 361 | CGCGCGCGCTGCTGCTCAGCTCCGGGACATCAATGCGCTGCTGCGCGGAGCGCTTGGC | 420 |
| Db | 336 | CGCGCGCGACTCGCTAACCACTCCGAAACTCAACATACGCTACTCGCGCAAAAACGTCTAAC | 2777 |
| QY | 421 | TGGCGCTGCGCGCGCTGCTCCCGCAACGGTAAAGCCAC | 457 |
| Db | 276 | TAAAGTAAACCGCGCTGCTCCTTACAGATTAACCAAC | 240 |
| RESULT 7 | | | |
| ID | ABQ47034/C | | |
| XX | ABQ47034 standard; DNA; 556 BP. | | |
| AC | ABQ47034; | | |
| XX | | | |
| DT | 12-JUL-2002 (first entry) | | |
| XX | | | |
| DE | Oligonucleotide for detecting cytosine methylation SEQ ID NO 33625. | | |
| KW | Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; | | |
| KW | drug; side effect; cancer; central nervous system; cardiovascular; | | |
| KW | gastrointestinal; respiratory system; single nucleotide polymorphism; | | |
| KW | SNP; cell differentiation; ds. | | |
| XX | | | |
| OS | Homo sapiens. | | |
| XX | | | |
| PN | WO200218632-A2. | | |
| XX | | | |
| PD | 07-MAR-2002. | | |
| XX | | | |
| PE | 01-SEP-2001; 2001WO-EP10074. | | |
| XX | | | |
| FR | 01-SEP-2000; 2000DE-1043826. | | |
| PR | 05-SEP-2000; 2000DE-1044543. | | |
| XX | | | |
| PA | (EPIG-) EPIGENOMICS AG. | | |
| XX | | | |
| PI | Olek A, Piepenbrock C, Berlin K, Guetig D; | | |
| XX | | | |
| DR | WPI; 2002-371829/40. | | |
| PT | Determining the degree of cytosine methylation in genomic DNA, useful | | |
| PT | for diagnosis and prognosis, comprises selective hybridization of | | |
| PT | amplicons from chemically treated DNA | | |
| XX | | | |
| PS | Claim 12; 56pp + Sequence Listing; 56pp; German. | | |
| XX | | | |
| CC | This invention describes a novel method for determining the degree of | | |
| CC | methylation of a particular cytosine in a motif 5'-CpG-3', present in a | | |
| CC | genomic sample of DNA. The sample is treated chemically to convert | | |
| CC | cytosine (C) but not methylated C, to uracil, then part of the genomic | | |
| CC | DNA that contains the target C is amplified to form a labeled amplicon. | | |
| CC | The amplicon is hybridised to two classes, each with at least one | | |
| CC | member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers | | |
| CC | and the degree of hybridisation to both classes is determined from the | | |
| CC | label on the amplicon. From the ratio of labels hybridised to the two | | |
| CC | classes of oligomers, the degree of methylation is calculated. The method | | |
| CC | is used: (i) for diagnosis and/or prognosis of side effects of | | |
| CC | therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders | | |
| CC | of the central nervous, cardiovascular, gastrointestinal and respiratory | | |
| CC | systems etc., particularly by detecting mutations or single nucleotide | | |
| CC | polymorphisms (SNP's), and (ii) for differentiation of cell or tissue | | |
| CC | types and for investigating cell differentiation. The method allows the | | |
| CC | methylation status of many C residues to be determined simultaneously. | | |

CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory
 CC systems etc., particularly by detecting mutations or single nucleotide
 CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
 CC types and for investigating cell differentiation. The method allows the
 CC methylation status of many C residues to be determined simultaneously.
 CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
 CC method for determining the degree of cytosine methylation described in
 CC the disclosure of the invention.

XX Sequence 556 BP; 57 A; 71 C; 241 G; 187 T; 0 other;

Query Match 65.3%; Score 298.4; DB 24; Length 556;
 Best Local Similarity 81.1%; Pred. No. 1.1e-41;
 Matches 347; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 26 GGCCCTTGGGAGCCCTGAGCCGAGAGCCGAGAGCCGAGAGCCGCTGCTGAGAGA 85
 DB 1 GGTTCGTGAGTATTGTTGGTTGTTAGAGCGGAGAGTGGAGTTCGTTGGTGAGA 60
 QY 86 CTGGGGGTGAGGTGCTCCGAGCGTACCAGCCCGGAGTACCTCCGCTCACACTCG 145
 61 TTGGGGGTGAGGTGCTCCGAGCGTACCAGCGTACCAGTATTTTCGTTTATTTTCG 120
 QY 146 GGCTGCACTCCCTGGGTGGCCCGGAGAGCGTGGCCCGGCTGAGAGATGGCGGGCG 205
 DB 121 GGTGTAGTATTTTGGGTGCTGCGAGAGTGGTTCGGGTGGAGAGATGGGGGGCG 180
 QY 206 GGAGACGGGGGCGGGGGGCGGCTGCTGACGTGAGAGAGCGCGGGGGCGGGCGG 265
 DB 181 GGAGACGGGGGCGGGGGGCGGCTGCTGACGTGAGAGAGCGCGGGGGCGGGCGG 240
 QY 266 GGGGCGCGCCCGGCTCTTAAAGCGCGCGAGCGCGAGAGTCTCTGTGGCGG 325
 DB 241 GGGGCGCGCTCCGTTTAAAGCGCGCGAGCGCGAGAGTCTCTGTGGCGG 300
 QY 326 CAGGCGGAGCGCCGGGGGAGACCGGAGACGTGAGAGCGCGCGCTGCTGAGTCCGGG 385
 DB 301 TAGGCGGAGGTTCGGGGGATAGTGAACCGTGAAGCGCGTGGTTCGTTGAGTTGGG 360
 QY 386 ACTCAACATGCGTGTGCGCGGAGAGCGTGTGAGCGCTGAGCGCGCTGCTGCA 445
 DB 361 ATTAAATATGCGTGTGCTGCGGAGAGCGTGTGAGCGTGTGCTGCTGTTTGTGA 420
 QY 446 CGGTAAG 453
 DB 421 CGGTAAG 428

--SUIT 5

1A7037/C

ABQ47037 standard; DNA; 556 BP.

AC ABQ47037;

DT 12-JUL-2002 (first entry)

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 33628.

XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.

XX Homo sapiens.

OS WO200218632-A2.

PD 07-MAR-2002.

XX 01-SEP-2001; 2001WO-EP10074.

XX 01-SEP-2000; 2000DE-1043826.

PR 05-SEP-2000; 2000DE-1044543.

XX (EPIC-) EPIGENOMICS AG.

PA Olek A, Piepenbrock C, Berlin K, Guetig D;

PI WPI; 2002-371829/40.

XX Determining the degree of cytosine methylation in genomic DNA, useful
 PT for diagnosis and prognosis, comprises selective hybridization of
 PT amplicons from chemically treated DNA

XX Claim 12; 56pp + Sequence Listing; 56pp; German.

CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridized to two classes, each with at least one
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 CC and the degree of hybridization to both classes is determined from the
 CC label on the amplicon. From the ratio of labels hybridized to the two
 CC classes of oligomers, the degree of methylation is calculated. The method
 CC is used: (i) for diagnosis and/or prognosis of side effects of
 CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory
 CC systems etc., particularly by detecting mutations or single nucleotide
 CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
 CC types and for investigating cell differentiation. The method allows the
 CC methylation status of many C residues to be determined simultaneously.
 CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
 CC method for determining the degree of cytosine methylation described in
 CC the disclosure of the invention.

XX Sequence 556 BP; 187 A; 241 C; 71 G; 57 T; 0 other;

Query Match 65.3%; Score 298.4; DB 24; Length 556;
 Best Local Similarity 81.1%; Pred. No. 1.1e-41;
 Matches 347; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 26 GGCCCTTGGGAGCCCTGAGCCGAGAGCCGAGAGCCGCTGCTGAGAGA 85
 DB 556 GGTTCGTGAGTATTGTTGGTTGTTAGAGCGGAGAGTGGAGTTCGTTGGTGAGA 497
 QY 86 CTGGGGGTGAGGTGCTCCGAGCGTACCAGCCCGGAGTACCTCCGCTCACACTCG 145
 DB 496 TTGGGGGTGAGGTGCTCCGAGCGTACCAGCGTACCAGTATTTTCGTTTATTTTCG 437
 QY 146 GGCTGCACTCCCTGGGTGGCCCGGAGAGCGTGGCCCGGCTGAGAGATGGCGGGCG 205
 DB 436 GGTGTAGTATTTTGGGTGCTGCGAGAGTGGTTCGGGTGGAGAGATGGGGGGCG 377
 QY 206 GGAGACGGGGGCGGGGGGCGGCTGCTGACGTGAGAGAGCGCGGGGGCGGGCGG 265
 DB 376 GGAGACGGGGGCGGGGGGCGGCTGCTGACGTGAGAGAGCGCGGGGGCGGGCGG 317
 QY 386 ACTCAACATGCGTGTGCGCGGAGAGCGTGTGAGCGCTGAGCGCGCTGCTGCA 445
 DB 361 ATTAAATATGCGTGTGCTGCGGAGAGCGTGTGAGCGTGTGCTGCTGTTTGTGA 137
 QY 446 CGGTAAG 453
 DB 136 CGGTAAG 129

| | | | |
|--|---|--|-----|
| Dp | | 301 GAGCGGCGAGGTGCCTCTGTGGCCGCGAGGCCGCGGCGACGACGCGTGTGAG | 360 |
| Qy | 361 | CGCGCCGCGTCCCTGTGAGCTCCGGGACTCAAC | 392 |
| | | | |
| Dp | 361 | CGCGCGGCTCGCTGCAGCTCCGGGACTCAAC | 392 |
| | | | |
| RESULT 3 | | | |
| ID | ABUJ34018 | standard, DNA, 5304 BP. | |
| XX | | | |
| XX | ABUJ34018; | | |
| AC | | | |
| XX | | | |
| DT | 26-MAR-2002 | (first entry) | |
| DE | | | |
| XX | | | |
| Human immune system associated gene SEQ ID NO: 1991. | | | |
| Human; immune system disease; cytosine methylation; antiasthmatic; antihistoneosclerotic; antianaemic; cyrosarctic; noctropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene; ds. | | | |
| KM | Homo sapiens. | | |
| XX | | | |
| XX | MO200200928-A2. | | |
| PD | | | |
| XX | 03-JAN-2002. | | |
| PP | | | |
| XX | 02-JUL-2001; 2001WO-EP07537. | | |
| PR | | | |
| XX | 30-JUN-2000; 2000DE-1032529. | | |
| PR | 01-SEP-2000; 2000DE-1043826. | | |
| PA | (EPIG-) EPIGENOMICS AG. | | |
| XX | | | |
| XX | Olek A, Piepenbrock C, Berlin K; | | |
| PI | | | |
| DR | WPI; 2002-130909/17. | | |
| PT | | | |
| Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation - | | | |
| s | | | |
| Claim 1; SEQ ID NO 1991, 32pp + Sequence Listing; German. | | | |
| XX | | | |
| The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention. | | | |
| Sequence 5304 BP; 1480 A; 152 C; 1219 G; 2453 T; 0 other; | | | |
| Query Match | 69.7%; Score 318.6; DB 24; Length 5304; | | |
| Best Local Similarity | 81.5%; Pred. No. 3.2e-45; | | |
| Matches 369; Conservative 0; Mismatches 84; Indels 0; Gaps 0; | | | |
| 1 AGAAGCAGAGGAGGAGGTAGAGCCCTTGCGGAGAGCCCTTGCGGAGGAGGCGG | 60 | | |
| AGAAGCAGAGGAGGAGGTAGAGTTTGTGGGTAGTTTGTGGTTTAGAGGCGG | 466 | | |
| AGGCGGAGAGCCGCTCGGTGAGAGCTGGGGGTGAGGTGCCGAGAGGTACCAGCGCC | 120 | | |
| AGGTTCGAGAGTTTCGTTGCGGTGAGATTGGGGGTGAGAGGTTCGAGAGGTATTTAGCGTC | 472 | | |
| GGAAGTACCTCCCGCTCACACCTCGGCTGCAGTTCCCTTGAGGTGGCGCGAGACGCTGG | 180 | | |

[illegible]

DR WPI, 1999-288306/24.
 XX Human alpha-7 neuronal nicotinic acetylcholine receptor and related
 PT polynucleotides
 XX Claim 1, Fig 4, 104pp; English.
 XX The present invention describes an isolated nucleotide sequence (1)
 CC encoding at least a portion of the human alpha-7 neuronal nicotinic
 CC acetylcholine receptor (alpha7-hnAChR). Also described are: (1) a
 CC peptide encoded by (1); (2) a vector comprising (1); (3) a host cell
 CC transformed with a vector of (2); (4) a polynucleotide comprising at
 CC least 15 nucleotides which hybridises under stringent conditions to at
 CC least a portion of (1); (5) a method for detection of a polynucleotide
 CC encoding alpha 7-hnAChR in a biological sample; and (6) a method for
 CC amplification of nucleic acid from a sample suspected of containing
 CC nucleic acid encoding alpha 7-hnAChR. The primers and probes from the
 CC present invention can be used on brain tissue and blood samples of
 CC humans suspected of suffering from schizophrenia, small cell lung
 CC carcinoma, breast cancer and nicotine-dependent illness. This is
 CC particularly useful for diagnosis of schizophrenia. Other illnesses
 CC that can be studied/diagnosed are epilepsy (e.g. juvenile myoclonic
 CC epilepsy) and Prader-Willi and Angelman's syndromes.
 .X Sequence 457 BP; 58 A; 145 C; 204 G; 50 T; 0 other;
 SQ
 Query Match 100.0%; Score 457; DB 20; Length 457;
 Best Local Similarity 100.0%; Pred. No. 3.5e-68;
 Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAAGCGAAGGAGAGAGTGAAGCTTGAGCCCTTGAGCCCTTGAGCCAGAGGCGG 60
 Db 1 AGAAGCGAAGGAGAGAGTGAAGCTTGAGCCCTTGAGCCCTTGAGCCAGAGGCGG 60
 QY AGGCGGAGAGCCGCTCGTGAAGTCTGGAGGCTGAGGCTGAGGCGGAGAGCGCC 120
 Db AGGCGGAGAGCCGCTCGTGAAGTCTGGAGGCTGAGGCTGAGGCGGAGAGCGCC 120
 QY 121 GGAAGTACCTCCGCTCACAACCTTGAGGCTGAGGCTGAGGCGGAGAGCGCTGG 180
 Db 121 GGAAGTACCTCCGCTCACAACCTTGAGGCTGAGGCTGAGGCGGAGAGCGCTGG 180
 QY 181 CCCGGGCTGAGAGGATGCGGCGGAGAGCGGCGGCGGCGGCGGCTGCTCACTGGAG 240
 Db 181 CCCGGGCTGAGAGGATGCGGCGGAGAGCGGCGGCGGCGGCGGCTGCTCACTGGAG 240
 QY 241 AGGCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCTCTTAAGGCGGCGAGCC 300
 Db 241 AGGCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCTCTTAAGGCGGCGAGCC 300
 QY 301 GAGCGGCGAGGCTGCTGTGAGCGGAGCGGCGGCGGCGGCGAGCGAGAGCTGGAG 360
 Db 301 GAGCGGCGAGGCTGCTGTGAGCGGAGCGGCGGCGGCGGCGAGCGAGAGCTGGAG 360
 QY 361 CGGCGCGGCTGCGTGAAGTCTGAGGCTGAGGCTGAGGCTGAGGCGGAGGCTGAGG 420
 Db 361 CGGCGCGGCTGCGTGAAGTCTGAGGCTGAGGCTGAGGCTGAGGCGGAGGCTGAGG 420
 QY 421 TGGGCGTGAAGGCTGCTCTGAGCGAGCGTAAAGCCAG 457
 Db 421 TGGGCGTGAAGGCTGCTCTGAGCGAGCGTAAAGCCAG 457

RESULT 2
 AAX56151
 ID AAX56151 standard; DNA; 392 BP.
 XX
 AC AAX56151;
 XX
 DT 15-JUL-1999 (first entry)
 XX
 DE Human alpha-7 nicotinic receptor nucleotide sequence fragment #8.
 XX

KW Human; alpha-7 nicotinic receptor; neuronal; hybridisation; probe;
 KW alpha-7 neuronal nicotinic acetylcholine receptor; schizophrenia;
 KW small cell lung carcinoma; breast cancer; nicotine-dependent illness;
 KW epilepsy; juvenile myoclonic epilepsy; Prader-Willi syndrome;
 KW Angelman's syndrome; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO920757-A2.
 XX
 PD 29-APR-1999.
 XX
 PF 15-OCT-1998; 98MO-US21762.
 XX
 PR 23-OCT-1997; 97US-0956518.
 XX
 PA (FREE/) FREEDMAN R.
 PA (LEON/) LEONARD S.
 XX
 PI Freedman R, Leonard S;
 XX
 DR WPI, 1999-288306/24.
 XX
 PT Human alpha-7 neuronal nicotinic acetylcholine receptor and related
 PT polynucleotides
 XX
 PS Claim 1, Fig 8; 104pp; English.
 XX
 CC The present invention describes an isolated nucleotide sequence (1)
 CC encoding at least a portion of the human alpha-7 neuronal nicotinic
 CC acetylcholine receptor (alpha7-hnAChR). Also described are: (1) a
 CC peptide encoded by (1); (2) a vector comprising (1); (3) a host cell
 CC transformed with a vector of (2); (4) a polynucleotide comprising at
 CC least 15 nucleotides which hybridises under stringent conditions to at
 CC least a portion of (1); (5) a method for detection of a polynucleotide
 CC encoding alpha 7-hnAChR in a biological sample; and (6) a method for
 CC amplification of nucleic acid from a sample suspected of containing
 CC nucleic acid encoding alpha 7-hnAChR. The primers and probes from the
 CC present invention can be used on brain tissue and blood samples of
 CC humans suspected of suffering from schizophrenia, small cell lung
 CC carcinoma, breast cancer and nicotine-dependent illness. This is
 CC particularly useful for diagnosis of schizophrenia. Other illnesses
 CC that can be studied/diagnosed are epilepsy (e.g. juvenile myoclonic
 CC epilepsy) and Prader-Willi and Angelman's syndromes.
 CC
 SQ Sequence 392 BP; 51 A; 122 C; 180 G; 39 T; 0 other;
 Query Match 85.8%; Score 392; DB 20; Length 392;
 Best Local Similarity 100.0%; Pred. No. 2.6e-57;
 Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAAGCGAAGGAGAGTGAAGCTTGAGCCCTTGAGGCGGCGGCGGCGGCGGCGG 60
 Db 1 AGAAGCGAAGGAGAGTGAAGCTTGAGCCCTTGAGGCGGCGGCGGCGGCGGCGG 60
 QY 61 AGGCGGAGAGCCGCTCGTGAAGTCTGGAGGCTGAGGCTGAGGCGGAGCGTACCGAGCC 120
 Db 61 AGGCGGAGAGCCGCTCGTGAAGTCTGGAGGCTGAGGCTGAGGCGGAGCGTACCGAGCC 120
 QY 121 GGAAGTACCTCCGCTCACAACCTTGAGGCTGAGGCTGAGGCGGCGGAGAGCTGGAG 180
 Db 121 GGAAGTACCTCCGCTCACAACCTTGAGGCTGAGGCTGAGGCGGCGGAGAGCTGGAG 180
 QY 181 CCCGGGCTGAGAGGATGCGGCGGAGAGCGGCGGCGGCGGCGGCTCTTAAGGCGGCGAG 240
 Db 181 CCCGGGCTGAGAGGATGCGGCGGAGAGCGGCGGCGGCGGCGGCTCTTAAGGCGGCGAG 240
 QY 241 AGGCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTCTTAAGGCGGCGAGCC 300
 Db 241 AGGCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTCTTAAGGCGGCGAGCC 300
 QY 301 GAGCGGCGAGGCTGCTGTGAGCGGAGCGGCGGCGGCGGCGGCGAGAGCTGGAG 360
 Db 301 GAGCGGCGAGGCTGCTGTGAGCGGAGCGGCGGCGGCGGCGGCGAGAGCTGGAG 360

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2003, 05:13:39 ; Search time 269 Seconds
(without alignments)
4586.034 Million cell updates/sec

Title: US-08-956-518a-94

Perfect score: 457

Sequence: 1 AGAAGCGAAGGAGAGGTAG.....CTCCTGCACGTTAAGCCAC 457

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

ched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N Geneseq 190un03.*
1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 457 | 100.0 | 457 | 20 | AA56144 |
| 2 | 392 | 85.8 | 392 | 20 | AA56151 |
| 3 | 318.6 | 69.7 | 5304 | 24 | AB134018 |
| 4 | 298.4 | 65.3 | 556 | 24 | AB047036 |
| 5 | 298.4 | 65.3 | 556 | 24 | AB047037 |
| 6 | 221.8 | 48.5 | 5304 | 24 | AB134019 |
| 7 | 212.4 | 46.5 | 556 | 24 | AB047034 |
| 8 | 212.4 | 46.5 | 556 | 24 | AB047035 |

| | | | | | | |
|----|------|------|--------|----|----------|---------------------|
| 9 | 127 | 27.8 | 1876 | 15 | AAV12197 | Human neuronal nic |
| 10 | 127 | 27.8 | 1876 | 18 | AA748239 | Neuronal nicotinic |
| 11 | 127 | 27.8 | 1876 | 24 | ABV73248 | Human neuronal NAC |
| 12 | 127 | 27.8 | 1876 | 24 | AB554875 | Human neuronal nic |
| 13 | 69.2 | 15.1 | 3861 | 14 | AAQ51543 | Lipopolysaccharide |
| 14 | 68.8 | 15.1 | 114955 | 20 | AA53491 | Human adenosine A1 |
| 15 | 67 | 14.7 | 600 | 24 | AB052496 | Oligonucleotide fo |
| 16 | 67 | 14.7 | 600 | 24 | AB052497 | Oligonucleotide fo |
| 17 | 66.2 | 14.5 | 1000 | 21 | AA02484 | Human colon cancer |
| 18 | 65.6 | 14.4 | 1127 | 21 | AA02477 | Human colon cancer |
| 19 | 65.6 | 14.4 | 114793 | 22 | AA08215 | Human genome from |
| 20 | 65.2 | 14.3 | 1337 | 20 | AA217263 | Human gene express |
| 21 | 65.2 | 14.3 | 114955 | 20 | AA53491 | Human adenosine A1 |
| 22 | 64.6 | 14.1 | 12733 | 24 | ABK98631 | Vector pEPER14 con |
| 23 | 64.6 | 14.1 | 12739 | 24 | ABK98592 | Vector pEPER14 cont |
| 24 | 64 | 14.0 | 3198 | 20 | AAK02974 | Human IL-1ra BAC c |
| 25 | 63.2 | 13.8 | 43058 | 24 | ABN97455 | Gene #3953 used to |
| 26 | 63.2 | 13.8 | 43058 | 24 | AB164982 | Lung cancer relate |
| 27 | 63.2 | 13.8 | 43058 | 24 | AB165219 | Lung cancer relate |
| 28 | 63 | 13.8 | 154746 | 24 | AA025519 | Human herpesvirus |
| 29 | 63 | 13.8 | 154746 | 24 | AA025519 | Human herpesvirus |
| 30 | 62 | 13.6 | 1964 | 24 | AB211268 | Human polynucleoti |
| 31 | 61.6 | 13.5 | 544 | 24 | AB024355 | Oligonucleotide fo |
| 32 | 61.6 | 13.5 | 544 | 24 | AB024355 | Oligonucleotide fo |
| 33 | 61.6 | 13.5 | 22976 | 20 | AA583426 | Genomic region con |
| 34 | 61.6 | 13.5 | 41936 | 24 | AB167924 | Ovary cancer relat |
| 35 | 61.4 | 13.4 | 2307 | 24 | ABK32842 | DNA encoding human |
| 36 | 61.2 | 13.4 | 1416 | 25 | AB220967 | Animal test kit ma |
| 37 | 60.6 | 13.3 | 320 | 21 | AAA38185 | Primer used in the |
| 38 | 60.6 | 13.3 | 1281 | 13 | AA032926 | HSV-1 (MGH-10) ICP |
| 39 | 60.2 | 13.2 | 712 | 24 | AB040858 | Oligonucleotide fo |
| 40 | 60.2 | 13.2 | 712 | 24 | AB040859 | Oligonucleotide fo |
| 41 | 59.8 | 13.1 | 434 | 22 | AA184343 | Human polynucleoti |
| 42 | 59.8 | 13.1 | 687 | 24 | ABQ19226 | Oligonucleotide fo |
| 43 | 59.8 | 13.1 | 687 | 24 | ABQ19227 | Oligonucleotide fo |
| 44 | 59.8 | 13.1 | 754 | 24 | ABQ40800 | Oligonucleotide fo |
| 45 | 59.8 | 13.1 | 754 | 24 | ABQ40801 | Oligonucleotide fo |

ALIGNMENTS

| | |
|---------|--|
| AA56144 | RESULT 1 |
| ID | AA56144 standard; DNA; 457 BP. |
| AC | AA56144; |
| XX | XX |
| XX | 15-JUL-1999 (first entry) |
| DT | XX |
| XX | Human alpha-7 nicotinic receptor nucleotide sequence fragment #1. |
| DE | XX |
| XX | Human; alpha-7 nicotinic receptor; neuronal; hybridisation; probe; |
| KW | Human; alpha-7 neuronal nicotinic acetylcholine receptor; schizophrenia; |
| KW | small cell lung carcinoma; breast cancer; nicotine-dependent illness; |
| KW | epilepsy; juvenile myoclonic epilepsy; Prader-Willi syndrome; |
| KW | Angelman's syndrome; PCR primer; ss. |
| XX | XX |
| OS | Homo sapiens. |
| XX | XX |
| PN | WO920757-A2. |
| PD | 29-APR-1999. |
| XX | XX |
| PF | 15-OCT-1998; 98WO-US21762. |
| XX | XX |
| PR | 23-OCT-1997; 97US-0956518. |
| XX | XX |
| PA | (FREE/) FREEDMAN R. |
| PA | (LEON/) LEONARD S. |
| XX | XX |
| PI | Freedman R, Leonard S; |
| XX | XX |

LOCATION: (745)..(747)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (750)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (752)
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FEATURE:
NAME/KEY: modified_base
LOCATION: (754)..(756)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (761)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (763)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (818)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (843)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (892)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (897)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (920)
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FEATURE:
NAME/KEY: modified_base
LOCATION: (941)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (993)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (995)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
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FEATURE:
NAME/KEY: modified_base
LOCATION: (1082)..(1084)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (1105)..(1107)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (1130)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (1147)

OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (1247)..(1248)
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FEATURE:
NAME/KEY: modified_base
LOCATION: (1261)
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FEATURE:
NAME/KEY: modified_base
LOCATION: (1485)
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NAME/KEY: modified_base
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FEATURE:
NAME/KEY: modified_base
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FEATURE:
NAME/KEY: modified_base
LOCATION: (1601)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (1605)
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FEATURE:
NAME/KEY: modified_base
LOCATION: (1635)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (1637)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (1654)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (1674)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (1695)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (1852)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (1866)..(1865)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (1968)..(1980)
OTHER INFORMATION: a, t, c, g, unknown or other

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US-10-349-836-11
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
Query Match 27.8%; Score 127; DB 12; Length 1876;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 321 GCGCGAGCGCCGAGCCCGGGCGAGCGAGCGAGCGCGCGCGCTCGTCGAGCT 380
Db 1 GCGCGAGCGCCGAGCCCGGGCGAGCGAGCGAGCGCGCGCGCTCGTCGAGCT 60
QY 381 CCGGGACTCAACATGCGCTGCTCGCCGGAGGCGCTGAGCTGCGCCGCTGCGCTC 440
Db 61 CCGGGACTCAACATGCGCTGCTCGCCGGAGGCGCTGAGCTGCGCCGCTGCGCTC 120
QY 441 CTGCACG 447
Db 121 CTGCACG 127

RESULT 5
US-10-017-161-1857
Sequence 1857, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentn Ver. 2.1
SEQ ID NO 1857
LENGTH: 3163
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: source
LOCATION: (1)..(3163)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(2963)
FEATURE:
NAME/KEY: modified_base
LOCATION: (556)..(655)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (658)..(669)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (671)..(697)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (704)..(707)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (709)..(736)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (739)..(743)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base

```

| | | | |
|----|------|--|------|
| QY | 121 | GGAGTACCTCCCTCACACCTCGAGGTGAGTTCCTGGATGGCCGCGAGACGCTGG | 180 |
| Dd | 4729 | GGAGATATTTTCGTTATATTTTCGGGTGTAGATTTTTCGATGTGTCTCGACAGCTTGG | 4788 |
| QY | 181 | CCCGGCTGAGAGATGCGGGGCGGGGCGGGGCGGGGCGGGGCTCTCATGCTGAG | 240 |
| Dd | 4789 | TTGGGGTTGAGAGGATGGGGGGGGGGGACGGGGCGGGGCTCGTTACGTGGAG | 4848 |
| QY | 241 | AGCGCGCGGGGGCGGGCGGGGCGCGCGCGCGCTCTTAAAGCGCGGAGCC | 300 |
| Dd | 4849 | AGCGCGGGGGGGGGCGGGCGGGGCGCGCTTCGTTTAAAGCGCGCGAGTC | 4908 |
| QY | 301 | GAGCGGCGAGGTGCTCTGTGTGGCCGCGAGCGCAGGCCCGGGCGACAGCCGAGACTGGAG | 360 |
| Dd | 4909 | GAGCGCGAGGTGTTTGTGTGCTAGAGCGTAGTTTCGGCGATAGTCGAGAGCTGGAG | 4968 |
| QY | 361 | CGCGCGGCTCGCTGCGAGCTCGGGAGCTCAACATGCGCTGTCTCGCGGGAGAGGCTGCGC | 420 |
| Dd | 4969 | CGCGTCGGTGTGTAGTTCGGGATTTAATAGCGTGTGTCGCGGAGAGCGTTTGT | 5028 |
| QY | 421 | TGCGCTGAGCGCGTGCCTCTGCACGGTAAAG | 453 |
| Dd | 5029 | TGCGCTTGCTCGCTCGTTTGTAGACGTTAAG | 5061 |

RESULT 2

```

US-10-311-455-1992/c
/ Sequence 1992, Application US/10311455
/ Publication No. US20030143606A1
/ GENERAL INFORMATION:
/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIEPENBROCK, Christian
/ APPLICANT: BEHLIN, Kurt
/ TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Expression of Cytosine Methyltransferase 1
/ TITLE OF INVENTION: Cytosine methylation
/ FILE REFERENCE: 5013.1014
/ CURRENT APPLICATION NUMBER: US/10/311,455
/ CURRENT FILING DATE: 2002-12-16
/ PRIOR APPLICATION NUMBER: PCT/EP01/07537
/ PRIOR FILING DATE: 2001-07-02
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 2424
/ SEQ ID NO 1992
/ LENGTH: 5304
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1992

```

| | | 48.5% | Score 221.8 | DB 12 | Length 5304 |
|---------|-----|-----------------------------|--|----------------|-------------|
| | | Best Local Similarity 67.8% | Pred. No. 3,5e-40 | | |
| Matches | 310 | Conservative | 0 | Mismatches 147 | Indels 0 |
| | | | | Gaps | 0 |
| QY | 1 | AGAA | CGCAAGGAGAGTAGAGCCTTGCGCTTTGGGCGAGCCCTTGCGCTTGCCAGAGCGCG | 60 | |
| Db | 696 | AAAA | CGCAAAAAAATAATAAAACTTAACCTTAACCAACCCCTTAACCTTAACCAAAAAACGG | 637 | |
| QY | 61 | AGGCG | AGAGCGCCGTCGCTGGTAGAGCTCGGGGTGAGAGTCCCGGAGGCTACCCGACGCC | 120 | |
| Db | 636 | AAAC | CGAAAAACCCGTCGATAAAACTAAAAATATAAAAAATCCCGAAAGGTACCAACGCC | 577 | |
| QY | 121 | GGGAG | TACCTCCCGCTCAACCTCGGGCTGCAGTTCCCTGGGTGGCCGCGCAGACGCTGG | 180 | |
| Db | 576 | GAAAT | ACTCCCGCTCAACCTCGAATCAAAATTCCTTAATAACCGCGCAAAAGCTTAA | 517 | |
| QY | 181 | CCCGG | GCTGAGAGGAGTGGCGGGGCGGGGACGGGGGCGGGGCGGGGCTCTCTACGTGGAG | 240 | |
| Db | 516 | CCCGA | ACTTAAAAATAAAAAACGAAACGAAACGAAACGAAACGAAACCTGTACCTTAAA | 457 | |

[illegible]

RESULT 3

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US-09-892-985-7
: Sequence 7, Application US/09892985
: Patent No. US2002011463A1
GENERAL INFORMATION:
APPLICANT: Eliot, Kathryn J.
            Ellis, Steven B.
            Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Heller Erman White & McAuillife
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/892,985
FILING DATE: 27-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/217,345
FILING DATE: 21-DEC-98
APPLICATION NUMBER: US 08/467,574
FILING DATE: 05-JUN-95
APPLICATION NUMBER: US 08/466,589,
FILING DATE: 05-JUN-95
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 73..1581
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-892-985-7

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Db 4669 AGGTCGAGAGTTCGTTCCGCTGAGATTGGGGGTCGAGGTCGTCGAGCGCTATTTCGCGTC 4722

Seq primer: RM1 TACGACTCACTATAGGAGA

Class: BAC ends

High quality sequence start: 25

High quality sequence stop: 160.

FEATURES
source
1. 1198
Location/Qualifiers

/organism="Gallus gallus"

/mol_type="genomic DNA"

/strain="Red Jungle Fowl"

/db_xref="taxon:9031"

/clone="CH261-138F22"

/sex="female"

/cell_line="UCD001, inbred 256"

/clone_id="CH261"

/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI; CH261 Female Chicken library - For library and clone ordering information: <http://www.chori.org/bacpac>"

BASE COUNT 29 a 748 c 341 g 35 t 45 others

ORIGIN

Query Match 19.0%; Score 87; DB 29; Length 1198;

Best Local Similarity 49.2%; Pred. No. 9.7e-06;

Matches 207; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

14 GAGTAAAGCTTGGCTTGGGACACCTTGGCTTGGCCAGAGGCGCGAGCCGAGAGCCC 73
675 GGG 616
74 GCTCGTGAAGACTGGGGGTTGGAGTGTGCGCCGAGCGTAAACCGAGCGCGGGAGTACTCC 133
615 GCGGG 556
134 GCTCACAACCTCGGGCTCAGTTCCCTGAGTGGCCCGAGACGCTGCGCCGGGCTGAGG 193
555 GGG 496
194 GATGGCGGGGGGGGAGCGGGGGCGGGGGCGTCTGTCACGTGGAAGGCGCGGGGGG 253
495 GCGGG 436
254 CGGG 313
435 CCGCGGG 376
314 CTTCTGTGGCGGAGCGAGCGCGCGGCGGACGAGCGTGAAGCGCGCGCGCTGCG 373
375 GCGCGGG 316
374 TGCAAGCTCCGGGACTCAATGCGCTGCTGCGCGGAGGCGTCTGCGCTGCGCGC 433
315 GCGGG 256
434 G 434
255 G 255

RESULT 15

CNS04CNH 549 bp DNA linear GSS 01-SEP-2000
LOCUS
DEFINITION
09J04 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION

AL284678.1 GI:8023072

KEYWORDS
GSS; genome survey sequence.

SOURCE

ORGANISM
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

1

AUTHORS

Roeest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Pizames, C., Wincker, P., Brothier, P., Querier, F., Saurin, W., and Weissbach, J.

Estimate of human gene number provided by genome-wide analysis

using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)

20296633

10835645

2

Roeest Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C., Pizames, C., Fischer, C., Bouneau, L., Billault, A., Querier, F., Saurin, W., Bernot, A., and Weissbach, J.

Characterization and repeat analysis of the compact genome of the

freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

10899143

3 (bases 1 to 549)

Genoscope.

Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr

This sequence is a single read and was generated as part of a large

scale clone-end sequencing project of the Tetraodon nigroviridis

genome. For more information, please take a look at

<http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

source

1. 549
/organism="Tetraodon nigroviridis"

/mol_type="genomic DNA"

/db_xref="taxon:99883"

/clone="09J04"

/clone_id="G"

/note="Genoscope sequence ID : COBG09DE02LP1-end : T7"

BASE COUNT

20 a 81 c 407 g 16 t 25 others

ORIGIN

Query Match 18.9%; Score 86.2; DB 29; Length 549;

Best Local Similarity 48.4%; Pred. No. 1.4e-05;

Matches 196; Conservative 13; Mismatches 196; Indels 0; Gaps 0;

10 GGGAGAGTGAAGCTTGGCTTGGGACACCTTGGCTTGGCCAGAGCGCGAGAGCCGAG 69
120 GGG 179
70 GCGCGTCCGTGAGACTGGGGGTTGAGTGGCCCGAGCGTACCGAGCGCGGAGTACC 129
180 GCGCGCGCGGG 239
130 TCCCGCTCAACCTCGGGCTGCAATTCCCTGGGTGGCGCGCGAGACGCTGACCCGGG 189
240 GSGCGCCCGGG 239
190 GAGGAGATGGCGGGGGGGGAGCGGGGGCGGGGGCGGCGCTGTGACTGTGAAGAGCGCG 249
300 CGGG 359
250 GGG 309
360 GGGCGGG 419
310 GGTGCTCTGTGCGCCAGCGGAGCGCGGGCGGAGCGGAGCGGAGCGTGAAGCGCGCGC 369
420 GGGGGSS 479
370 TCGCTGAGCTCCGGGACTCAATGCGCTGCTGCGCGGGAGCG 414
480 TSGGGAGAGCGCGATGTGCGCTGTGCGCTGAGAGGGGAGCG 524

Search completed: September 7, 2003, 15:14:42
Job time : 2272 secs

| | |
|-----------------------|--|
| DEFINITION | 603181651F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5245812 5', |
| ACCESSION | NRNA sequence. |
| VERSION | BI917899 |
| KEYWORDS | EST. |
| SOURCE | EST. BI917899.1 GI:16181580 |
| ORGANISM | Homo sapiens (human) |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. |
| TITLE | 1 (bases 1 to 651) |
| JOURNAL | NIH-MGC http://mgs.nci.nih.gov/. |
| COMMENT | Unpublished. National Institutes of Health, Mammalian Gene Collection (MGC) Contact: Robert Strausberg, Ph.D. Email: cga@bbs-rtm1.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LLAM11620 row: e column: 13 High quality sequence stop: 647. Location/Qualifiers 1..651 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5245812" /lab_host="DH10B" /clone_11b="NIH_MGC_121" /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note this is a NIH_MGC Library." |
| BASE COUNT | 137 a 188 c 182 g 144 t |
| ORIGIN | |
| Query Match | 19.3%; Score 88; DB 12; Length 651; |
| Best Local Similarity | 100.0%; Pred. No. 6.8e-06; |
| Matches | 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Qy | 354 CGTGGAGCGCCCGGCTGCTGCAAGCTCCGGAGCTCAACATGCGCTGCGCGGAGAGC 413 |
| Db | 1 CGTGGAGCGCCCGGCTGCTGCAAGCTCCGGAGCTCAACATGCGCTGCGCGGAGAGC 60 |
| Qy | 414 GTCTGGCTGGCGGCTGGCGCGGCTGCTCC 441 |
| Db | 61 GTCTGGCTGGCGGCTGGCGCGGCTGCTCC 88 |
| RESULT 13 | |
| LOCUS | BX403654 1103 bp mRNA linear EST 15-MAY-2003 |
| LOCUS | BX403654 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBAA0072H12 |
| ACCESSION | BX403654 |
| VERSION | 3-PRIME, mRNA sequence. |
| KEYWORDS | EST. BX403654.1 GI:30762430 |
| SOURCE | EST. |
| ORGANISM | Homo sapiens (human) |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. |
| TITLE | 1 (bases 1 to 1103) |
| JOURNAL | L1.W.B., Gruber, C., Jeesee, J., and Polayes, D. |
| COMMENT | Full-length cDNA libraries and normalization |

JOURNAL COMMENT

Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seq@genoscope.cns.fr, Web : "www.genoscope.cns.fr"
Library was constructed by Life Technologists, a division of Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/
Invitrogen Corporation 1600 Faraday Avenue Menlo Park CA 94025
location/Qualifiers

FEATURES
source

1..1103
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOBA007ZHI2"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

BASE COUNT
194 a 34 c 310 g 269 t 296 others

ORIGIN

Query Match 19.0%; Score 87; DB 13; Length 1103;
Best Local Similarity 35.6%; Pred.No. 9.7e-06;
Matches 103; Conservative 80; Mismatches 106; Indels 0; Gaps 0;

Oy 144 CGAGCTGCACTTCCTCGGTGGCCGCCGAGACGCTGCCCCGGGCTGCAGGATGCGGGG 203
|||
Db 209 SGGGARRRRAGGG 268
CGGGAGCGGG 263
204 |||
Db 269 GGG 328
264 GGGGGCGCGCGCGCGGCTCTTTAAAGCGCGGAGCCGAGCGGAGGTGCTTGTCG 323
329 GGGGGSSSGCCCCCCCCSSSSSSSSGGGGGGGGGGGGGGGGGGGGGGGGGGGG 388
Oy 324 GCAGGGCGAAGCCCCGGGGCGACAGCCAGACTGAAGCGCGCGGCTGCTGCACTTCG 383
Db 389 GGG 448
384 GGACTCAACATGGCGTCTCGCGGGAGGGGCTGTGGCGCTGGCG 432
449 SSS 497

RESULT 14
CC190008/c CC190008/c

LOCUS
DEFINITION
CC190008 1198 bp. DNA linear GSS 08-MAY-2003
CH261-13BF22.RM1.1 CH261 Gallus gallus genomic clone CH261-13BF22,
genomic survey sequence.

ACCESSION
CC190008

VERSION
CC190008.1 GI:30434823

KEYWORDS
GSS.

SOURCE
Gallus gallus (chicken)

ORGANISM
Gallus gallus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1198)
Kemtitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
Warren, W., Graves, T., Wardis, E. and Wilson, R.
Unpublished
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Insert Length: 18200 Std Error: 0.00

Db 1093 GGCCSCCCC 1102

RESULT 10
AL530299
LOCUS
DEFINITION
AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
CDNA clone CS0DD007YP05 5-PRIME, mRNA sequence.

ACCESSION
AL530299
VERSION
AL530299.2 GI:31068132
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
COMMENT
On Feb 13, 2001 this sequence version replaced gi:12793792.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
7646.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DD007CH03QPLcluster=7646.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/InvitrogenCorporation1600
Faraday Avenue Genoscope Sequence ID : CS0DD007CH03QPL.
Location/Qualifiers
1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DD007YP05"
/issue_type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 258 a 326 c 319 g 273 t 25 others

ORIGIN

Query Match 19.7%; Score 90.2; DB 9; Length 1201;
Best Local Similarity 95.0%; Pred. No. 2.8e-06;
atches 114; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 328 GGCGACAGCCCGGCGACAGCGAGCGAGCGCGCGCTGCGAGCTCCGGAC 387
Db 62 GGCGACAGCCCGGCGACAGCGAGCGAGCGCGCGCTGCGAGCTCCGGAC 120

QY 388 TCACATGCGCTCTCTGCGCGGAGCGCTGCTGCGCGCGCGCTGCTCTTACG 447
Db 121 TCACATGCGCTCTCTGCGCGGAGG-TNCTGCTGCGCGCGCGCGCTGCTCTTACG 179

RESULT 11
AG128304
LOCUS
DEFINITION
AG128304
ACCESSION
AG128304.1 GI:16657469
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Toroki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of library PTB
Unpublished
2 (bases 1 to 1023)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Toroki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsukuba, Ibaraki, Japan, 305-8565, Japan
(E-mail: chimpes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the RAD process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1. 1023
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-139G20.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 9 a 196 c 649 g 56 t 113 others

ORIGIN

Query Match 19.4%; Score 88.6; DB 29; Length 1023;
Best Local Similarity 47.0%; Pred. No. 5.2e-06;
Matches 199; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

QY 10 GGAGAGGTAGACCTGTGCTTTGGGAGCCCTTGGCCGACAGGCGGAGCCGAGA 69
Db 269 GGGNNNGGG 328

QY 70 GCGGCTGTGTGAGACTGTGGGGGTGTGAGAGTCCCGAGACCTTACCGCGGAGTAC 129
Db 329 GGNNGGGGGGGGGNNNGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGNN 388

QY 130 TCCGCTACACCTCGGCTGCTGCTTCCCTGGGTGCGCGAGACGCTGCGCCGGCTG 189
Db 369 GGGGGGNNNGGG 448

QY 190 GAGGATGCGCGGCGGAGCGGAGCGGCGGCGGCGCTGTCACTGTGAGAGCGCGCG 249
Db 449 GGGGGGNNNGGG 508

QY 250 GGGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 309
Db 509 GGG 568

QY 310 GGTGCTCTGTGAGCGCGAGCGCGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCG 369
Db 569 GGNNNNGGG 628

QY 370 TCGTGAAGCTCCCGGAGCTCAACATGCGCTGCTGCGCGGAGCGCTGTGCGCGCTG 429
Db 629 GCGGNNNGGGGGCGGNNNGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 688

QY 430 CCG 432
Db 689 CCG 691

RESULT 12
B1917899
LOCUS
B1917899 651 bp mRNA linear EST 16-OCT-2001

ACCESSION BX415111
 VERSION BX415111.1
 KEYWORDS GI:30765470
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 982)
 AUTHORS Li, W. B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT
 CONTACT Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 EMAIL: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CC0CNP004BB10Qp1.
 JURES Location/Qualifiers
 SOURCE 1..982

| | | | | | |
|------------|-------|-------|-------|------|------------|
| BASE COUNT | 177 a | 257 c | 323 g | 18 t | 207 others |
| ORIGIN | | . | | | |

| | | | | |
|-----------------------|------------------|-------------------|----------|------------|
| Query Match | 20.3% | Score 92.6 | DB 13 | Length 982 |
| Best Local Similarity | 32.4% | Pred. No. 1.1e-06 | | |
| Matches 143 | Conservative 117 | Mismatches 179 | Indels 2 | Gaps 1 |

[illegible]

RESULT 9

| FEATURES | LOCATION/Qualifiers |
|------------|--|
| GENOSCOPE | 1203 bp DNA linear GSS 26-JUL-1999 |
| LOCUS | CNS015Y4 |
| DEFINITION | Drosophila melanogaster genome survey sequence T7 end of BAC BACN15E10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence. |
| ACCESSION | AL106054 |
| VERSION | AL106054.1 GI:5619805 |
| KEYWORDS | GSS. |
| SOURCE | Drosophila melanogaster (fruit fly) |
| ORGANISM | Drosophila melanogaster |
| | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. |
| REFERENCE | 1 (bases 1 to 1203) |
| AUTHORS | Genoscope. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqret@genoscope.cns.fr |
| COMMENT | - Web : www.genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration of this European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaut at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelosBAC11. |

| | | | | | | | | | | |
|------------|-----|---|-----|---|-----|---|-----|---|-----|--------|
| BASE COUNT | 154 | a | 274 | c | 380 | g | 158 | t | 237 | others |
| ORIGIN | | | | . | | | | | | |

| | | | | | | |
|----|---|--------------|-----------|-----------------|--------------|---------|
| | Query Match | 19.9% | Score 91; | DB 29; | Length 1203; | |
| | Best Local Similarity | 38.1%; | Pred. | No. 2e-06; | | |
| | Matches 164; | Conservative | 84; | Mismatches 180; | Indels 2; | Gaps 1; |
| Dy | 30 TTGGGCAAGCCCTGTGCCTGTGCACAGAGCGAGGCCGAGACCCTGTCGGTGTGAAGACTGG | 89 | | | | |
| Db | 673 TTTCCGSGSGSSSSSbSSSSSCSSCCCCCSCSSSGGGGGCGCCCGSGSGGGGGGGGGGGG | 732 | | | | |
| Dy | 90 GGGTGAGAGTGTCCCGGAGCGTACCCAGCGCCGGAGTACTCCCGTTCACACTTCGGGCT | 149 | | | | |
| Db | 733 GGGGGGGGGSGGCGCGSGCYCCCCCCCCCCCCCCCCCCCCCCCCCGSSGSGSGGG | 792 | | | | |
| Dy | 150 GCAATTCCCTGTGGGTGCGCGCGCGAGAAGCGTATGCCCGGCTGTGAAGGATATG--CGAGCGGG | 207 | | | | |
| Db | 793 GGSGSGGCGCGGGGGGGGGSGCGGGCCCCCGGGGGGGCCSSGGGGGGGGCCCCSGGSGCC | 852 | | | | |
| Dy | 208 GACGGGGGCGGGGCGGGGCTGTCACTGTGAAGAGCGCGGGGGCGGGCGGGGCGGGG | 267 | | | | |
| Db | 853 CCGSGCGGGGGGGGGGGMCCCSCCGSGGGGGGSSCGSSSGGGGGGGGGGGGGGGGG | 912 | | | | |
| Dy | 268 GCCTCGGCCCCGGCTCTTTAAGCGCGCGCACCGAGCGGGCGGAAGTGGCTCTTGTGGCCGCA | 327 | | | | |
| Db | 913 GNGGGGGGGNVSgGSGGVVGGVVVGgSMGGMGMVAvgGGGGMSrCMGGvSSSS | 972 | | | | |
| Dy | 328 GGGCGAGGCGCCGGGGCGACAGCGTAGTGAAGCGCGCGCTGCTGTGTGACATTCGGAGAC | 387 | | | | |
| Db | 973 VSGSSSSSGGGGSSSGGGGGGvGGCGVMGGGGGGGGCCSSSGGGGGGGMGMNMGGGG | 1032 | | | | |
| Dy | 388 TC AACATGCGCTGTGCGCCGGAGGGGTGTGCTGCGCGTGTGCGCGCTCTCTGCAGC | 447 | | | | |
| Db | 1033 GMSSGGSSSGGGGGGGGGGGGGGGCCCCSSSSSSGSSrCCrCGCCCGGCGCCCCSSGGCC | 1092 | | | | |

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| FEATURES | Db | RESULT 6 | EST |
|------------|--|------------------------|-----------------|
| LOCUS | 162 | GCCTGACCGCGTCTCTCTGACG | 187 |
| DEFINITION | BX174871 | 222 bp | mRNA |
| ACCESSION | BX374871 | 222 bp | linear |
| VERSION | BX374871 | 222 bp | EST 08-MAY-2000 |
| KEYWORDS | BX374871.1 | GI:30448361 | EST |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Eutheria; Primates; Carnivora; Hominiidae; Homo. | | |
| AUTHORS | Li, W.B., Gruber, C., Jessup, J., and Polayes, D. | | |
| TITLE | Full-length cDNA libraries and normalization | | |
| JOURNAL | Unpublished | | |
| COMMENT | Contact: Genoscope | | |
| | Genoscope - Centre National de Sequencage | | |
| | BP 191 91006 Evry cedex - France | | |
| | Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr | | |
| | Library was constructed by Life Technologies, a division of | | |
| | Invitrogen. This sequence belongs to sequence cluster 7646.r For | | |
| | more information about this cluster, see | | |
| | http://www.genoscope.cns.fr/ | | |
| | cdg-bin/cluster.cdg1seq=CS0DC004BA06QPLcluster=7646.r. Contact : | | |
| | Feng Liang Email : fliang@lifetech.com URL : | | |
| | http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 | | |
| | Paradise Avenue Genoscope sequence ID : CS0DC004BA06QPL. | | |
| | Location/Qualifiers | | |

| Query | Local Similarity | Score | DB | Length |
|---|------------------|-------|-------|--------|
| 302 AGCGGCGAGTGCCTCTGTGTGGCCGAGCGCAGGCCCGGCGACACCGAGACGTGAGAC | 87.0% | 96.2 | 21.1% | 222 |
| 40 ACCGGTCGGAATTCCTCCGAGATTCGAGCGGAGCGCCCGGGCGACA--GAGACGTGGAGC | 87.0% | 92.9 | 21.1% | 222 |
| 362 GCGCGGCTGCTGCTGAGAGCTCCGGGACTCAACATGTGGCTGTCCGGGAGCGCTTGCT | 87.0% | 92.9 | 21.1% | 222 |
| 98 GCGCGGCTGCTGCTGAGAGCTCCGGGACTCAACATGTGGCTGTCCGGGAGCGCTTGCT | 87.0% | 92.9 | 21.1% | 222 |
| 422 GCGCGTGGCGCGTGCCTCTGTCAGC | 87.0% | 92.9 | 21.1% | 222 |
| 157 GCGCGTGGCGCGTGCCTCTGTCAGC | 87.0% | 92.9 | 21.1% | 222 |

Query Match

set Local Similarity 87.0% Pred. No. 2.9e-07

atches 127; Conservative 1; Mismatches 15; Indels 3; Gaps 2

BASE COUNT

45 a 62 c 76 g 35 t

ORIGIN

1/organism="Homo sapiens"

2/mol_type="mRNA"

3/db_xref="taxon:9606"

4/clone="CSODC004YA12"

5/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"

6/clone_id="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"

7/prime="1st strand cdna was primed with a NotI-oligo(dT)"

8/prime="Five prime end enriched, double-strand cdna was"

9/digested="with NotI and cloned into the NotI and EcoR V"

10/sites="of the pCMVSPORT 6 vector. Library was normalized."

RESULT 7

1201 bp mRNA linear EST 05-MAY-2005

DEFINITION BX365176 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

LOCUS BX365176.1 GI:30382886

ACCESSION BX365176

VERSION BX365176.1

KEYWORDS

| SOURCE | FEATURES | COMMENT |
|---|---|--|
| <p>ORGANISM</p> <p>Homosapiens (human)</p> <p>Homosapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.</p> <p>REFERENCE</p> <p>1 (bases 1 to 1201)</p> <p>Li, W. B., Gruber, C., Jessee, J. and Polayes, D.</p> <p>Full-length cDNA libraries and normalization</p> <p>Unpublished</p> <p>Contact: Genoscope</p> <p>Genoscope - Centre National de Sequencage</p> <p>BP 191 91006 EVRY cedex - France</p> <p>Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr</p> <p>Library was constructed by life technologies, a division of</p> <p>Invitrogen. This sequence belongs to sequence cluster 4244.f For</p> <p>more information about this cluster, see</p> <p>http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSA10152C02QPl&cluster=4244.f. Contact :</p> <p>Feng Liang Email : fliang@lifetech.com URL :</p> <p>http://fulllength.invitrogen.com/InvitrogenCorporation 1600</p> <p>Faraday Avenue Genoscope sequence ID : CSA10152C02QPl.</p> | <p>FEATURES</p> <p>SOURCE</p> <p>1..1201</p> <p>Location/Qualifiers</p> <p>Location="Homosapiens"</p> <p>mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="CSOD1058YA02"</p> <p>/cissue_type="PLACENTA"</p> <p>/clone_lib="Homosapiens PLACENTA COT 25-NORMALIZED"</p> <p>/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Fivd prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."</p> | <p>JOURNAL</p> <p>113 a 538 c 264 g 110 t 156 others</p> |

| Query March | 20.4% | Score 93 | DB 13 | Length 1201 |
|-----------------------|-----------------|---|----------|-------------|
| Best Local Similarity | 47.5% | Pred. No. 9.2e-07 | | |
| Matches 198 | Conservative 22 | Mismatches 197 | Indels 0 | Gaps 0 |
| QY | 32 | GGGAGCCCCCTGGGCTGTGGCCAGAGCGCGAGGCCGAGAGCCCGCTCGGTGGAGACTGGGG | 91 | |
| Db | 554 | GGGGGGCGGGCGGGGGCGCGCGCGCGCGCGCGAGAGCGCGAGAGCGCGGGGGGGGGGGGGGG | 495 | |
| QY | 92 | GTGAGAGTGCCTCCGAGAGGTATCCAGCGCCGGGAGTACTCTCCCGCTACACACTCGGGCTGC | 151 | |
| Db | 494 | GGGGGGCGCGGG | 435 | |
| QY | 152 | AGTTCCTGGGTGGGCTCCGCGAGAGCGTGTGGCCCGGGGTGGAGAGATGTGCGGGGCGAGACG | 211 | |
| Db | 434 | GGGGGGGGCGAGAGGGGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | 375 | |
| QY | 212 | GGGGCGGGGGCGGGGGCTGCTACGTGAGAGAGCGCGCGGGGGGGGGGGGGGGGGGGGGGGCGC | 271 | |
| Db | 374 | GG | 315 | |
| QY | 272 | GGCGCCCGGCTCTTAAGCGCGCGAGCGCGGAGCGGGCGGAGAGGCGCTGTGGCCCGAGGGCG | 331 | |
| Db | 314 | GG | 255 | |
| QY | 332 | CAGGCCCGGGCGAGCAGCGAGACGTGAGCGCGCGGCTCGCTCAGCTCCGGGACTCA 391 | | |
| Db | 254 | GGGGAGGA | 195 | |
| QY | 392 | CATCGCGTGCCTCGCGGGAGAGCGCTGTGGCTGTGGCTCGCCCGCTTCCTCTGCACGG 448 | | |
| Db | 194 | ASGGCGGG | 138 | |

5'-GACTAGTTTATGATCGGAGCGGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

BASE COUNT 198 a 251 c 247 g 212 t

Query Match 27.1%; Score 124; DB 13; Length 908;
Best Local Similarity 100.0%; Pred. No. 5e-12;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 CGCAGCGCAGCGCCCGGCGACAGCCGAGACGTGAGCGCGCGCTGCGTGCAGCTCCG 383
DB 1 CGCAGCGCGCAGCGCCCGGCGACAGCCGAGACGTGAGCGCGCGCTGCGTGCAGCTCCG 60
QY 384 GGACTCAACATGCGCTGCTGCGCGGAGCGCTGCGCTGCGCGCTGCGCTCTG 443
61 GGACTCAACATGCGCTGCTGCGCGGAGCGCTGCGCTGCGCGCTGCGCTCTG 120
QY 444 CACG 447
DB 121 CACG 124

RESULT 4

LOCUS B0070018 1080 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT_6660390 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5922336
5', mRNA sequence.

ACCESSION B0070018
VERSION B0070018.1 GI:19899064
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgc.ncl.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LCM2089 row: b column: 01
High quality sequence stop: 142.
Location/Qualifiers

FEATURES

Source

1. 1080
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5922336"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

BASE COUNT 259 a 286 c 244 g 290 t 1 others

Query Match 24.9%; Score 113.8; DB 13; Length 1080;
Best Local Similarity 94.4%; Pred. No. 2.7e-10;
Matches 118; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 322 GCCGACGCGCAGCGCCCGGCGACAGCCGAGACGTGAGCGCGCGCTGCTGCAGCTC 381
DB 1 GCCGACGCGCAGCGCCCGGCGACAGCCGAGACGTGAGCGCGCGCTGCTGCAGCTC 60
QY 382 CGGAGCTCAACATGCGCTGCTGCGGAGCGCTGCGCTGCGCGCGCTGCTGC 441
DB 61 CGGAGCTCAACATGCTGCTGCGCGGAGCATGTGCGCTGCGCGCTGCTGC 120
QY 442 TGCAC 446
DB 121 TGCAC 125

RESULT 5

LOCUS BX403124 1034 bp mRNA linear EST 13-MAY-2003
DEFINITION BX403124 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC0041A12 5-PRIME, mRNA sequence.

ACCESSION BX403124
VERSION BX403124.1 GI:30611171
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Li W.B., Gruber C., Jessee J. and Polyes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7646.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1DC001ZG090P1&cluster=7646.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1DC001ZG090P1.
Location/Qualifiers

FEATURES

Source

1. 1034
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC0041A12"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMSFORP 6 vector. Library was normalized."

BASE COUNT 213 a 298 c 288 g 218 t 17 others

Query Match 22.3%; Score 101.8; DB 13; Length 1034;
Best Local Similarity 84.2%; Pred. No. 3e-08;
Matches 123; Conservative 1; Mismatches 21; Indels 1; Gaps 1;

QY 302 ACCGCGAGTCTCTGTGCGCGCAGCGCGCGCGCGACCGAGACGTGAGC 361
DB 43 ACCGCGCGAGTCTCTGTGCGCGCAGCGCGCGCGCGACCGAGACGTGAGC 102
QY 362 GCGCGCGCTGCTGCACTCGCGGACTCAACATGCGCTGCGCGGAGCGCTGCGCT 421
DB 103 GCGCGCGCTGCTGCACTCGCGGACTCAACATGCGCTGCGCGGAGCGCTGCGCT 161

FEATURES High quality sequence stop: 404.

source

```

1. 1125
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6337441"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/note="Organ: Brain; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
Note: this is a NIH_MGC Library."

```

BASE COUNT 192 a 482 c 242 g 209 t

Query Match 28.7%; Score 131; DB 13; Length 1125;
 Best Local Similarity 100.0%; Pred. No. 3.2e-13;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 317 CTGTGCGCGAGCGAGCGCCCGGCGACAGCGAGCGCGCGGCTGCTGC 376
DB 71 CTGTGCGCGAGCGAGCGCCCGGCGACAGCGAGCGCGCGGCTGCTGC 130
QY 377 AGCTCCGGAGCTCAACATGCGTCTGCGCGGAGCGCTGCTGCGCTGCG 436
DB 131 AGCTCCGGAGCTCAACATGCGTCTGCGCGGAGCGCTGCTGCGCTGCG 190
QY 437 GCTCTGCGACG 447
DB 191 GCTCTGCGACG 201

```

RESULT 2
 LOCUS B0894356 1084 bp mRNA linear EST 16-AUG-2002
 DEFINITION AGENCOURT_8725920 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6338722
 5' mRNA sequence.
 ACCESSION B0894356
 VERSION B0894356.1 GI:22286370
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
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 High quality sequence stop: 482.

FEATURES

source

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1. 1084
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/mol_type="mRNA"
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/clone="IMAGE:6338722"
/tissue_type="neuroblastoma, cell line"

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/lab_host="DH10B (phage-resistant)"
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/note="Organ: Brain; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
Note: this is a NIH_MGC Library."

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BASE COUNT 232 a 335 c 287 g 229 t 1 others

Query Match 28.2%; Score 129; DB 13; Length 1084;
 Best Local Similarity 100.0%; Pred. No. 6.9e-13;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 319 GTGGCGCGAGCGAGCGCCCGGCGACAGCGAGCGCGCGGCTGCTGCAG 378
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QY 379 CTCCGGAGCTCAACATGCGTCTGCGCGGAGCGCTGCTGCGCTGCGCG 438
DB 61 CTCCGGAGCTCAACATGCGTCTGCGCGGAGCGCTGCTGCGCTGCGCG 120
QY 439 TCCTGCGACG 447
DB 121 TCCTGCGACG 129

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RESULT 3
 LOCUS BUI49265 908 bp mRNA linear EST 03-SEP-2002
 DEFINITION AGENCOURT_8443358 lupski sympathetic_trunk Homo sapiens cDNA clone IMAGE:6192234 5' mRNA sequence.
 ACCESSION BUI49265
 VERSION BUI49265.1 GI:22662797
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
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FEATURES

source

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/sex="male"
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/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/clone_lib="lupski_sympathetic_trunk"
/note="Vector: pCMV-SPORT (Life Technologies); Site: 1: NotI; Site: 2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCAAGCGCTCG-3' and

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2003, 05:33:14 / Search time 2268 Seconds
(without alignments)
4897.331 Million cell updates/sec

Title: US-08-956-518A-94

Sequence: 1 AGAAGCGACGAGAGGTAG.....CTTCCTGACGGTAAAGCCAC 457

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

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1: em_estda.*
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3: em_estin.*
4: em_estmu.*
5: em_estov.*
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7: em_estro.*
8: em_hc.*
9: gb_est1.*
10: gb_est2.*
11: gb_hc.*
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13: gb_est4.*
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15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pin.*
20: em_gss_vit.*
21: em_gss_fun.*
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23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_tro.*
26: em_gss_phg.*
27: em_gss_vxl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 129 | 28.2 | 1084 | 13 | BO894356 AGENCOURT |
| 3 | 124 | 27.1 | 908 | 13 | BU149265 AGENCOURT |
| 4 | 113.8 | 24.9 | 1080 | 13 | BO070018 AGENCOURT |

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|----|-------|------|------|----|----------|
| 5 | 101.8 | 22.3 | 1034 | 13 | BK403124 |
| 6 | 96.2 | 21.1 | 222 | 13 | BK374871 |
| 7 | 93 | 20.4 | 1201 | 13 | BK365176 |
| 8 | 92.6 | 20.3 | 982 | 13 | BK415111 |
| 9 | 91 | 19.9 | 1203 | 29 | CNS01514 |
| 10 | 90.2 | 19.7 | 1201 | 9 | AL530299 |
| 11 | 88.6 | 19.4 | 1023 | 29 | AG128304 |
| 12 | 88 | 19.3 | 651 | 12 | BK197899 |
| 13 | 87 | 19.0 | 1103 | 13 | BK403654 |
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| 15 | 86.2 | 18.9 | 549 | 29 | CNS04041 |
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| 24 | 83.8 | 18.3 | 1050 | 13 | BO716109 |
| 25 | 83.6 | 18.2 | 1065 | 13 | BO681076 |
| 26 | 83.4 | 18.2 | 811 | 12 | BI956687 |
| 27 | 83 | 18.2 | 932 | 29 | CNS00720 |
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| 31 | 82.4 | 18.0 | 1080 | 28 | AQ093056 |
| 32 | 82.2 | 18.0 | 440 | 13 | BK403888 |
| 33 | 82 | 17.9 | 776 | 29 | CNS0109Y |
| 34 | 81.8 | 17.9 | 800 | 12 | BG780621 |
| 35 | 81.8 | 17.9 | 888 | 29 | AG030591 |
| 36 | 81.8 | 17.9 | 1061 | 13 | EX391246 |
| 37 | 81.6 | 17.9 | 1003 | 29 | AG159111 |
| 38 | 81.6 | 17.8 | 836 | 28 | AZ185303 |
| 39 | 81.4 | 17.8 | 857 | 29 | AG061653 |
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| 41 | 81.2 | 17.8 | 925 | 29 | CNS0091P |
| 42 | 81.2 | 17.8 | 942 | 29 | AG120142 |
| 43 | 81.2 | 17.8 | 932 | 29 | CNS0072Q |
| 44 | 81 | 17.7 | 1158 | 29 | CC251504 |
| 45 | 80.8 | 17.7 | | | |

ALIGNMENTS

RESULT 1
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AGENCOURT_8695252 NIH_MGC_47 Homo sapiens CDNA clone IMAGE:6377441
LOCUS
DEFINITION
VERSION
ACCESSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
EST.
BU148759.1 GI:22662291

REFERENCE
1 (bases 1 to 1125)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS
NIH-MGC <http://mgi.nci.nih.gov/>
TITLE
JOURNAL
COMMENT
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Found through the I.M.A.G.E. Consortium/LINL at:
<http://image.llnl.gov>
Plate: LICM2561 row: d column: 18
High quality sequence start: 54

High quality sequence start: 54

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>
 Series: IRAX Plate: 69 Row: C Column: 18
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21536283.

FEATURES

SOURCE

Location/Qualifiers

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 /db_xref="taxon:9606"
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CDS

BASE COUNT 380 a 530 c 495 g 405 t
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 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Db | 1 | CGTGGAGCGCGCGGCTGCTGTCAGACTCCGGGACTCAACATGCGCTGCGCGGAGGC | 60 |
| QY | 414 | GTCGTGGCTGGCGCTGGCGCGCTGCTCTGTCACG | 447 |
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Search completed: September 7, 2003, 14:36:43
 Job time : 2504 secs

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Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 GGGCCGAGGCGGAGGCGGCGGAGACGCTGAGAGCCGCGGCTGCTGACGCT 380
DB 1 GGGCCGAGGCGGAGGCGGCGGAGACGCTGAGAGCCGCGGCTGCTGACGCT 60
QY 381 CCGGACTCAACATCGCTGCTGCGGAGGCGCTGAGGCTGCGGCGGCTGCTC 440
DB 61 CCGGACTCAACATCGCTGCTGCGGAGGCGCTGAGGCTGCGGCGGCTGCTC 120
QY 441 CTGCACG 447
DB 121 CTGCACG 127

RESULT 14
LOCUS HSARA7A 2087 bp mRNA linear PRI 01-JUN-1994
DEFINITION H.sapiens mRNA for neuronal nicotinic acetylcholine receptor
alpha-7 subunit.
ACCESSION X70297.1 GI:496606
KEYWORDS neuronal nicotinic acetylcholine receptor alpha-7 subunit.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Peng,X., Katz,M., Gerzanich,V., Anand,R. and Lindstrom,J.
AUTHORS Human alpha 7 acetylcholine receptor: cloning of the alpha 7
TITLE subunit from the SH-SY5Y cell line and determination of
JOURNAL pharmacological properties of native receptors and functional alpha
MEDLINE 7 homeomers expressed in Xenopus oocytes
PUBMED 94195283
Wol. Pharmacol. 45 (3), 546-554 (1994)
8145738
2 (bases 1 to 2087)
Katz,M.
REFERENCE Direct Submission
AUTHORS Submitted (04-FEB-1993) M. Katz, Univ of Pennsylvania School of
TITLE Medicine, Dept of Neuroscience, 36th & Hamilton Walk, Rm 235
JOURNAL Stemmler Hall, Philadelphia, PA 19104, USA
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Best Local Similarity 96.1%; Pred. No. 2.4e-08;
Matches 146; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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DB 67 TGGAGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 126
QY 416 CTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 447
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RESULT 15
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DEFINITION Homo sapiens, clone MGC:45359 IMAGE:5245812, mRNA, complete cds.
ACCESSION BC037571
VERSION BC037571.1 GI:22902222
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1810)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2002) National Institutes of Health, Mammalian
MEDLINE Gene Collection (MGC), Cancer Genomics Office, National Cancer
PUBMED Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
CONTACT: nisc.mgc@nih.gov
NHI-MGC Project URL: http://mgc.nci.nih.gov
CONTACT: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Akhter,N., Ayala,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Latic,P., Legaspi,R.,
Maduro,O.L., Masliah,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stancipop,S., Thomas,P.J., Touchman,J.W.,
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| | | | |
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| Db | 121 CTGCACG 127 | | |
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| LOCUS | AR282833 | 1876 bp | DNA linear PAT 10-APR-2003 |
| DEFINITION | Sequence 11 from patent US 6524789. | | |
| ACCESSION | AR282833 | | |
| VERSION | AR282833.1 GI:29719625 | | |
| KEYWORDS | . | | |
| SOURCE | Unknown. | | |
| ORGANISM | Unclassified. 1 (bases 1 to 1876) Elliott,K.J. and Harpold,M.M. Human neuronal nicotinic acetylcholine receptor compositions and methods employing same Patent: US 6524789-A 11 25-FEB-2003; Location/Qualifiers 1..1876 /organism="unknown" | | |
| JOURNAL FEATURES | | | |
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| Db | 61 CGGGACTCAACATCGCTGCTCGCGGGAGGCGTCTGACTTGCGCTGACCGCGTCGCTC 120 | | |
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| Db | 121 CTGCACG 127 | | |
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| DEFINITION | Sequence 11 from Patent EPI295945. | | |
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| TITLE | AX719088.1 GI:29891591 | | |
| ABSTRACT | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | | |
| REFERENCE AUTHORS | Elliott,K.J. and Harpold,M.M. Human neuronal nicotinic acetylcholine receptor compositions and methods employing same Patent: EP 1295945-A 11 26-MAR-2003; MERCK & CO. INC. (US) | | |
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| DB | 121 | CTGCGACG 127 | | | |
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| LOCUS | Human nicotinic acetylcholine receptor alpha7 subunit precursor, | | | | |
| DEFINITION | RNA, complete cds. | | | | |
| ACCESSION | U62436 | | | | |
| VERSION | U62436.1 | | | | |
| KEYWORDS | GI:1458119 | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1876) | | | | |
| AUTHORS | Elliot, K.J., Ellis, S.B., Berckhan, K.J., Urrutia, A., Chavez-Notiega, L.E., Johnson, E.C., Velicelebi, G. and Harpold, M.M. Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits | | | | |
| TITLE | J. Mol. Neurosci. 7 (3), 217-228 (1996) | | | | |
| JOURNAL | J. Mol. Neurosci. 7 (3), 217-228 (1996) | | | | |
| MEDLINE | 97062879 | | | | |
| PUBMED | 8906617 | | | | |
| REFERENCE | 2 (bases 1 to 1876) | | | | |
| AUTHORS | Elliot, K.J. | | | | |
| TITLE | Direct Submision | | | | |
| JOURNAL | Submitted (28-JUN-1996) Kathryn J. Elliot, SIBIA Neurosciences, Inc., 505 Coast Blvd. So., La Jolla, CA 92037, USA | | | | |
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RESULT 7
AR055255 1876 bp DNA linear PAT 29-SEP-1999

LOCUS AR055255
DEFINITION Sequence 7 from patent US 5837489.
ACCESSION AR055255
VERSION AR055255.1 GI:5980832
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 1876)
TITLE Elliott,K.J., Ellis,S.B. and Harpold,M.M.
HUMAN NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR AND CELLS
TRANSFORMED WITH SAME DNA AND mRNA ENCODING AN-SUBUNIT OF
JOURNAL Patent: US 5837489-A 7 17-NOV-1998;
FEATURES
LOCATION/Qualifiers
source 1..1876
E COUNT 369 a 553 c 530 g 423 t 1 others
GIN

Query Match 27.8%; Score 127; DB 6; Length 1876;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 GGCCGAGGCGGAGCCCGGCGAGCCGAGAGCTGGAGCGCGCGCTCGTGCAGCT 380
DB 1 GGCCGAGGCGGAGCCCGGCGAGCCGAGAGCTGGAGCGCGCGCTCGTGCAGCT 60

QY 381 CCGGAGCTCAACATGCGTCTGCTCCGCGGAGCGCTGCTGCGCTGCGCGCTC 440
DB 61 CCGGAGCTCAACATGCGTCTGCTCCGCGGAGCGCTGCTGCGCTGCGCGCTC 120

QY 441 CTGCACG 447
DB 121 CTGCACG 127

RESULT 8
AR071403 1876 bp DNA linear PAT 18-FEB-2000

LOCUS AR071403
DEFINITION Sequence 7 from patent US 5910582.
ACCESSION AR071403
VERSION AR071403.1 GI:7222291
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 1876)
TITLE Elliott,K.J., Ellis,S.B. and Harpold,M.M.
HUMAN NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR COMPOSITIONS AND
METHODS EMPLOYING SAME
JOURNAL Patent: US 5910582-A 7 08-JUN-1999;
FEATURES
LOCATION/Qualifiers
source 1..1876
E COUNT 369 a 553 c 530 g 423 t 1 others
GIN

Query Match 27.8%; Score 127; DB 6; Length 1876;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 GGCCGAGGCGGAGCCCGGCGAGCCGAGAGCTGGAGCGCGCGCTCGTGCAGCT 380
DB 1 GGCCGAGGCGGAGCCCGGCGAGCCGAGAGCTGGAGCGCGCGCTCGTGCAGCT 60

QY 381 CCGGAGCTCAACATGCGTCTGCTCCGCGGAGCGCTGCTGCGCTGCGCGCTC 440
DB 61 CCGGAGCTCAACATGCGTCTGCTCCGCGGAGCGCTGCTGCGCTGCGCGCTC 120

QY 441 CTGCACG 447
DB 121 CTGCACG 127

DB 121 CTGCACG 127

RESULT 9
AR173187 1876 bp DNA linear PAT 17-DEC-2001

LOCUS AR173187
DEFINITION Sequence 7 from patent US 6303753.
ACCESSION AR173187
VERSION AR173187.1 GI:17912678
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 1876)
TITLE Elliott,K.J., Ellis,S.B. and Harpold,M.M.
HUMAN NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR COMPOSITIONS AND
METHODS EMPLOYING SAME
JOURNAL Patent: US 6303753-A 7 16-OCT-2001;
FEATURES
LOCATION/Qualifiers
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E COUNT 369 a 553 c 530 g 423 t 1 others
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Query Match 27.8%; Score 127; DB 6; Length 1876;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 381 CCGGAGCTCAACATGCGTCTGCTCCGCGGAGCGCTGCTGCGCTGCGCGCTC 440
DB 61 CCGGAGCTCAACATGCGTCTGCTCCGCGGAGCGCTGCTGCGCTGCGCGCTC 120

QY 441 CTGCACG 447
DB 121 CTGCACG 127

RESULT 10
AR224030 1876 bp mRNA linear PAT 26-SEP-2002

LOCUS AR224030
DEFINITION Sequence 11 from patent US 6440681.
ACCESSION AR224030
VERSION AR224030.1 GI:23332638
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 1876)
TITLE Elliott,K.J., Ellis,S.B. and Harpold,M.M.
METHODS FOR IDENTIFYING AGONISTS AND ANTAGONISTS FOR HUMAN NEURONAL
NICOTINIC ACETYLCHOLINE RECEPTORS
JOURNAL Patent: US 6440681-A 11 27-AUG-2002;
FEATURES
LOCATION/Qualifiers
source 1..1876
E COUNT 369 a 553 c 530 g 423 t 1 others
GIN

Query Match 27.8%; Score 127; DB 6; Length 1876;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 GGCCGAGGCGGAGCCCGGCGAGCCGAGAGCTGGAGCGCGCGCTCGTGCAGCT 380
DB 1 GGCCGAGGCGGAGCCCGGCGAGCCGAGAGCTGGAGCGCGCGCTCGTGCAGCT 60

QY 381 CCGGAGCTCAACATGCGTCTGCTCCGCGGAGCGCTGCTGCGCTGCGCGCTC 440
DB 61 CCGGAGCTCAACATGCGTCTGCTCCGCGGAGCGCTGCTGCGCTGCGCGCTC 120

| DB | 14736 | AGCGCGAAGCCCGCGTGGTGAACACTGCGGGGTGAAGTCCCGAGACGTAACCAAGGCC | 14676 | | |
|------------|--|---|-------|--------|-----------------|
| QY | 121 | GGAGATACCTCCCGCTCAACACTTGGCGTGAAGTTCTTGGGTGGCCCGAGACGCTGG | 180 | | |
| DB | 14676 | GGAGATACCTCCCGCTCAACACTTGGCGTGAAGTTCTTGGGTGGCCCGAGACGCTGG | 14617 | | |
| QY | 181 | CCCGGGCTGAGAGGANTGGCGGGGAGCGGGGAGCGGGGCGGGGGCTGTCACGTGGAG | 240 | | |
| DB | 14616 | CCCGGGCTGAGAGGANTGGCGGGGAGCGGGGAGCGGGGCGGGGGCTGTCACGTGGAG | 14557 | | |
| QY | 241 | AGCGCGCGGGGAGCGGGGAGCGGGGAGCGCGCGCGGCTCTTAAAGCGCGAGGCC | 300 | | |
| DB | 14556 | AGCGCGCGGGGAGCGGGGAGCGGGGAGCGCGCGCGGCTCTTAAAGCGCGAGGCC | 14497 | | |
| QY | 301 | GAGCGCGAGGTGCTCTGTGGCCGAGCGCGAGCGCGGAGCGAGCCCGAGCGAGCGTGGAG | 360 | | |
| DB | 14496 | GAGCGCGAGGTGCTCTGTGGCCGAGCGCGAGCGCGGAGCGAGCGCGAGCGAGCGTGGAG | 14433 | | |
| QY | 361 | CGCGCGCGGCTGCTGTCAGCTCCGGGACTCAACATGCGCTGCTGCGGGAGGCGTGGCG | 420 | | |
| DB | 14436 | CGCGCGCGGCTGCTGTCAGCTCCGGGACTCAACATGCGCTGCTGCGGGAGGCGTGGCG | 14377 | | |
| QY | 421 | TGGCGCTGCGCGCGCTGCTCTCTGACGAGTAAGCCAC | 457 | | |
| DB | 14376 | TGGCGCTGCGCGCGCTGCTCTCTGACGAGTAAGCCAC | 14340 | | |
| RESULT 3 | AF029837 | 392 bp | DNA | linear | PRI 16-DEC-1998 |
| LOCUS | AF029837 | | | | |
| DEFINITION | Homo sapiens alpha 7 neuronal nicotinic receptor gene, promoter region. | | | | |
| ACCESSION | AF029837 | | | | |
| VERSION | AF029837.1 | | | | |
| KEYWORDS | GI:3757792 | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | |
| AUTHORS | Gault, J., Robinson, M., Berger, R., Drebing, C., Logel, J., Hopkins, J., Moore, T., Jacobs, S., Meriwether, J., Choi, K.J., Kim, E.J., Walton, K., Bulting, K., Davis, A., Brees, C., Freedman, R., and Leonard, S. | | | | |
| TITLE | Genomic organization and partial duplication of the human alpha7 neuronal nicotinic acetylcholine receptor gene (CHRNA7) | | | | |
| JOURNAL | Genomics 52 (2), 173-185 | | | | |
| MEDLINE | 99000837 | | | | |
| REFERENCE | 9782083 | | | | |
| AUTHORS | 2 (bases 1 to 392) | | | | |
| TITLE | Leonard, S., Gault, J., Logel, J., Drebing, C., Robinson, M., Berger, R., Brees, C., Davis, A., Hopkins, J., and Freedman, R. | | | | |
| JOURNAL | Direct Submission | | | | |
| FEATURES | Submitted (15-OCT-1997) Psychiatry, University of Colorado Health Sciences Center, 4200 E. 9th Ave., Denver, CO 80262, USA | | | | |
| SOURCE | Location/Qualifiers | | | | |
| | 1..392 | | | | |
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| | /chromosome="15" | | | | |
| | /map="15q14; between D1S1031 and D1S1360" | | | | |
| | /cclone="CHRNA7-P" | | | | |
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| ORIGIN | promoter | | | | |
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| DB | Best Local Similarity | 100.0%; Fred. No. 2.8e-46; | | | |
| | Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | |
| | 1 AGAAGCGAAGGAGAGCTAGAGCTGGCTTTGGGAGAGCCCTGGCTGGGCGAGAGCGCG | | | | |
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| | | | | |
|-----------------------|--|--|---|----------------------------|
| OY | | 61 | AGGCCGAAGCCCGCTGGTGGAACTGAGGGGTGGAGTGCCCGGAGGATACCAGACGC | 120 |
| Dd | | 61 | AGGCCGAAGCCCGCTGGTGGAACTGAGGGGTGGAGTGCCCGGAGGATACCAGACGC | 120 |
| OY | | 121 | GGAGATACTCCGCTCAACCTCGGGCTGCAGTTCCCTGGGTGGCCGCGCAGAAGCTGG | 180 |
| Dd | | 121 | GGAGATACTCCGCTCAACCTCGGGCTGCAGTTCCCTGGGTGGCCGCGCAGAAGCTGG | 180 |
| OY | | 181 | CCCCGGCTGGAGGATGGCCGGGGCGGGGACCGGGGGCGGGGGCTTCGTACGTTGAG | 240 |
| Dd | | 181 | CCCCGGCTGGAGGATGGCCGGGGCGGGGACCGGGGGCGGGGGCTTCGTACGTTGAG | 240 |
| OY | | 241 | AGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGCGCGCGCTCTTAAGAGGGCGGACCC | 300 |
| Dd | | 241 | AGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGCGCGCGCTCTTAAGAGGGCGGACCC | 300 |
| OY | | 301 | GAGCGCGAGGTGCTCTGTGTGGCCGACAGCCCGGGCGACAGCCGAGACGTTGAG | 360 |
| Dd | | 301 | GAGCGCGAGGTGCTCTGTGTGGCCGACAGCCCGGGCGACAGCCGAGACGTTGAG | 360 |
| OY | | 361 | CGCGCGGCTGCTGTCAGACTCCGGGACTCAAC | 392 |
| Dd | | 361 | CGCGCGGCTGCTGTCAGACTCCGGGACTCAAC | 392 |
| RESULT 4 | | | | |
| .AX346920 | | | | |
| LOCUS | AX346920 | . | 5304 bp | DNA linear PAT 01-FEB-2002 |
| DEFINITION | Sequence 1991 from Patent WO0200928. | | | |
| VERSION | AX346920 | | | |
| ACCESSION | AX346920.1 | GI:18494806 | | |
| KEYWORDS | | | | |
| SOURCE | | | | |
| ORGANISM | | | | |
| REFERENCE | | | | |
| AUTHORS | 1 | | | |
| TITLE | Olek A., Piepenbrock C. and Berlin K. | | | |
| JOURNAL | Diagnosis of diseases associated with the immune system Patent: WO 0200928-A 1991 03-JAN-2002; Epigenomics AG (DE) | | | |
| FEATURES | | | | |
| source | | | | |
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| | /db_xref="taxon:32630"; | | | |
| | /note="Chemically treated genomic DNA (Homo sapiens)" | | | |
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| Best Local Similarity | 81.5%; Pred. No. 2.9e-36; | | | |
| Matches | 369; Conservative 0; Mismatches 84; Indels 0; Gaps 0; | | | |
| OY | 1 | AGAACGCAAGGAGAGTAGAGCTTGCCCTTGGGACCCCTGGCCTGGCCAGAGGCGCG | 60 | |
| Dd | 4609 | AGAACGTAAGGAGAGTAGAGTTGGTTTTGGGTAGTTTTGGTTGGTTAAGAGGCGCG | 4668 | |
| OY | 61 | AGGCCGAGAGCCCGCTCGGTGGAGACTGGGGGGTGGAGTCCCGGAGCGTACCAGCGCC | 120 | |
| Dd | 4669 | AGGTGGAAGATTCTTGGTGGAGATTGGGGGTGGAGGTGTTCCGAGCGTATTAGCGTC | 4728 | |
| OY | 121 | GGAGATACTCCGCTCACACTTGGGGCTCAGTTCCTGGGTGGCGCGCAGACGCTGG | 180 | |
| Dd | 4729 | GGAGATACTTTCGTTATAATTTTCGGGTGTAAGTTTTTGGGTGTGTGAGACGTTGG | 4788 | |
| OY | 181 | CCCCGGCTGGAGGATGGCGGGGGCGGGGACCGGGGGCGGGGGCTTCGTACGTTGAG | 240 | |
| Dd | 4789 | TTCCGGATTGGAAGGATGGGGGGCGGGGACGCGGGGCGGGGGCTTCGTTACGTGAG | 4848 | |
| OY | 241 | AGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGCGCGCGCTCTTAAGAGGGCGGACCC | 300 | |
| Dd | 4849 | AGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGCGCGCTTCTTAAGAGGGCGGACGTC | 4908 | |

Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
 Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
 Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
 Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
 Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
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 Kamat, A., Karatas, A., Kells, C., Larocque, K., Lamazares, R.,
 Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,
 Maclean, C., Macdonald, P., Major, J., Margulis, N., Matheis, L.,
 McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Menus, L.,
 Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
 Notbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
 Oliver, J., Peterson, K., Phunhkhang, P., Pierre, N., Pollara, V.,
 Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
 Roman, J., Rosetti, M., Roy, A., Santos, R., Schaner, S., Schupbach, R.,
 Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N.,
 Straus, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
 Submitted (10-MAY-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On May 10, 2002 this sequence version replaced gi:18693427.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information
 Project name: LI0937
 Center project name: LI0937
 Center clone name: 636_P_14

----- FEATURES
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Location/Qualifiers
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 /db_xref="taxon:9606"
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 466..476
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 3398..3738
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 3743..6334
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 6339..6468
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 repeat_region /rpt_family="(CCCCG)n" 16447..16557
 repeat_region /rpt_family="MIR" 16631..16665
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Query Match 99.6%; Score 455.4; DB 9; Length 227506;
 Best Local Similarity 99.8%; Pred. No. 4,9e-56;
 Matches 456; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAAGCGAGGAGAGGTAGAGCTTGAGCTTGAGCGAGCCCTTGAGCGAGAGCGCG 60
 Db 14796 AGAAGCGAGGAGAGGTAGAGCTTGAGCTTGAGCGAGCCCTTGAGCGAGAGCGCG 14737
 QY 61 AGCGCGAGAGCGCGCTCGGTGAGAGTGGGGGGGAGGTGCGCGGAGCGTACCGAGCGCC 120

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| Qy | 61 | AGGCGCCAGAGACCCCGCTTCGCTGGAGAGATGGGGGTGAGGTGCCCGAGCGTACCCAGCGCC | 120 | |
| Db | 128708 | AGGCGCCAGAGACCCCGCTTCGCTGGAGAGATGGGGGTGAGAGGTGCCCGAGCGTACCCAGCGCC | 128767 | |
| Qy | 121 | GGGAGTACCTCCCGCTCACACCTCGGGGTGAGATTCCCTGGGGTGGCCGAGACGGCTGG | 180 | |
| Db | 128768 | GGGAGTACCTCCCGCTCACACCTCGGGGTGAGATTCCCTGGGGTGGCCGAGACGGCTGG | 128827 | |
| Qy | 181 | CCGGGCTTGGAGGAGATGGCGGGGCGGGAGCGGGGGCGGGGCTCGTCACTGGAG | 240 | |
| Db | 128828 | CCGGGCTTGGAGGAGATGGGGGGGGCGGGAGCGGGGGCGGGGCTCGTCACTGGAG | 128887 | |
| Qy | 241 | AGCGCGCGGGGGCGGGGCGGGGGCGGGCGCGCGCTCTTTAAAGGGCGCGAGCC | 300 | |
| Db | 128888 | AGCGCGCGGGGGCGGGGCGGGGGCGGGCGCGCGCTCTTTAAAGGGCGCGAGCC | 128947 | |
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| Db | 128948 | GAGCGCGAGGTCTCTTGCGCCGAGCGAGGCGCCGGGCGACAGCCGAGAGCTGGAG | 129007 | |
| Qy | 361 | CGGCGCGGCTCGCTGAGCTCCGGGAGCTCAATGCGTGCCTCCCGGAGAGCGTCTGGC | 420 | |
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| Oy | 4211TGGCGCTGGCCGCGTCGTGCCTCGACGGGAAAGCCAC | 457 |
| Db | 129068 TGGCGCTGGCCGCGTCGTGCCTCGACGGGAAAGCCAC | 129104 |
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| LOCUS | AC079969/c | |
| ACCESSION | AC079969 | |
| VERSION | AC079969.5 | GI:20522205 |
| KEYWORDS | HTG. | |
| SOURCE | Homo sapiens (human) | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | |
| REFERENCE | 1 (bases 1 to 227506) | |
| AUTHORS | Birren,B., Linton,L., Nusbaum,C. and Lander,E. | |
| TITLE | Homo sapiens chromosome 15, clone RP11-636P14 | |
| JOURNAL | Unpublished | |
| REFERENCE | 2 (bases 1 to 227506) | |
| AUTHORS | Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Barina,N., Bastien,V., Bedalov,F., Boguslavsky,I., Boukhgalter,B., Brown,A., Burtsev,G., Campopiano,A., Castle,A., Chepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dekarello,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Harford,A., Horton,L., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Larocque,K., Lamazares,R., Landers,T., Lecheczy,J., Levine,R., Liu,C., Liu,G., Macdonald,P., Marguis,N., McCarthy,M., McEwan,P., McKernan,K., McSheeters,R., Meldrum,J., Menue,L., Mihova,T., Mlenga,V., Morrow,J., Murphy,I., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pletre,N., Plisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R., Rogov,P., Roehman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Souzaez,C., Spencer,B., Strange-Thomann,N., Stojanovic,N., Strausz,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M. | |
| TITLE | Direct Submission | |
| JOURNAL | Submitted (20-SEP-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA | |
| REFERENCE | 3 (bases 1 to 227506) | |
| AUTHORS | Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barina,N., Bastien,V., Boguslavsky,I., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.T., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., Dekarello,K., Dewar,K., Diaz,J.S., Dodge,S., Fato,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Larocque,K., Lamazares,R., Landers,T., Lecheczy,J., Levine,R., Liu,G., McLennan,C., MacDonald,P., Major,J., Marguis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrum,J., Menue,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunhkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnuppock,R., Seaman,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., ToPham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zemek,L., Zimmer,A. and Zody,M. | |
| TITLE | Direct Submission | |
| JOURNAL | Submitted (16-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA | |
| REFERENCE | 4 (bases 1 to 227506) | |
| AUTHORS | Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., | |

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2003, 05:26:09 ; Search time 2500 Seconds

(without alignments)
7478.280 Million cell updates/sec

Title: US-08-956-518A-94

Perfect score: 457

Sequence: 1 AGAAGCGAGAGAGAGGTAG.....CTCCTGACCGTTAAGCCAC 457

Scoring table: IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database :

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2: gb_hg:*
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17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
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23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pln:*
35: em_hg_rod:*
36: em_hg_tam:*
37: em_hg_vtc:*
38: em_sy:*
39: em_hg_hum:*
40: em_hg_mus:*
41: em_hg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
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| 2 | 455.4 | 99.6 | 227506 | 9 AC079969 | AC079969 Homo sapi |
| 3 | 392 | 85.8 | 332 | 9 AF029837 | AF029837 Homo sapi |
| 4 | 318.6 | 69.7 | 5304 | 6 AX346920 | AX346920 Sequence |
| 5 | 221.8 | 48.5 | 5304 | 6 AX346921 | AX346921 Sequence |
| 6 | 133.8 | 29.3 | 2107 | 9 AF486623 | AF486623 Macaca mu |
| 7 | 127 | 27.8 | 1876 | 6 AR055255 | AR055255 Sequence |
| 8 | 127 | 27.8 | 1876 | 6 AR071403 | AR071403 Sequence |
| 9 | 127 | 27.8 | 1876 | 6 AR173187 | AR173187 Sequence |
| 10 | 127 | 27.8 | 1876 | 6 AR224030 | AR224030 Sequence |
| 11 | 127 | 27.8 | 1876 | 6 AR282833 | AR282833 Sequence |
| 12 | 127 | 27.8 | 1876 | 6 AX719088 | AX719088 Sequence |
| 13 | 127 | 27.8 | 1876 | 9 HS062436 | HS062436 Human nico |
| 14 | 121.6 | 26.6 | 2087 | 9 HSARA7A | HSARA7A Homo sapi |
| 15 | 94 | 20.6 | 1810 | 9 BC037571 | BC037571 Homo sapi |
| 16 | 82.2 | 18.0 | 219952 | 2 AC084804 | AC084804 Mus muscu |
| 17 | 81.6 | 17.9 | 1393 | 11 PM1H12G | PM1H12G Penicilli |
| 18 | 81.2 | 17.8 | 141534 | 2 AP003685 | AP003685 Oryza sat |
| 19 | 80.2 | 17.5 | 155680 | 2 AC120887 | AC120887 Oryza sat |
| 20 | 78.8 | 17.2 | 81767 | 2 AC012929 | AC012929 Homo sapi |
| 21 | 78.6 | 17.2 | 64207 | 2 AC024002 | AC024002 Homo sapi |
| 22 | 78.6 | 17.2 | 146743 | 2 AP003518 | AP003518 Oryza sat |
| 23 | 78.2 | 17.1 | 971 | 11 PM1285B | PM1285B Penicilli |
| 24 | 78 | 17.0 | 78220 | 2 AC024266 | AC024266 Homo sapi |
| 25 | 77.8 | 17.1 | 65523 | 2 AC023212 | AC023212 Homo sapi |
| 26 | 77.4 | 16.9 | 885 | 11 PM7F8G | PM7F8G Penicilli |
| 27 | 76.8 | 16.8 | 63087 | 2 AC023446 | AC023446 Homo sapi |
| 28 | 76.6 | 16.8 | 113141 | 2 AC093919 | AC093919 Oryza sat |
| 29 | 76 | 16.6 | 129506 | 2 AC136100 | AC136100 Rattus no |
| 30 | 75.4 | 16.5 | 120091 | 2 AC012684 | AC012684 Homo sapi |
| 31 | 75.4 | 16.5 | 144979 | 2 AC016280 | AC016280 Homo sapi |
| 32 | 74.8 | 16.4 | 87283 | 2 AC022856 | AC022856 Homo sapi |
| 33 | 74.6 | 16.3 | 149454 | 2 AC013648 | AC013648 Homo sapi |
| 34 | 74.4 | 16.3 | 976 | 11 PM12D6G | PM12D6G Penicilli |
| 35 | 74 | 16.2 | 1052 | 11 PM2H12B | PM2H12B Penicilli |
| 36 | 73.8 | 16.1 | 11305 | 8. OSAS35061 | OSAS35061 Oryza sat |
| 37 | 73.8 | 16.1 | 159790 | 2 AP004786 | AP004786 Oryza sat |
| 38 | 73.8 | 16.1 | 220389 | 2 BX324177 | BX324177 Danio rex |
| 39 | 73.6 | 16.1 | 75628 | 2 AC021793 | AC021793 Homo sapi |
| 40 | 73.6 | 16.1 | 164520 | 2 AC020738 | AC020738 Homo sapi |
| 41 | 73.4 | 16.1 | 303091 | 2 AC084799 | AC084799 Mus muscu |
| 42 | 73 | 16.0 | 1094 | 11 PM7G11B | PM7G11B Penicilli |
| 43 | 73 | 16.0 | 167624 | 2 AC143286 | AC143286 Macaca mu |
| 44 | 72.8 | 15.9 | 76734 | 2 AC023218 | AC023218 Homo sapi |
| 45 | 72.4 | 15.8 | 114639 | 9 AC100810 | AC100810 Homo sapi |

ALIGNMENTS

RESULT 1
AC058803
LOCUS AC058803 203493 bp DNA linear PRI 11-DEC-2001
DEFINITION Homo sapiens chromosome 15, clone RP11-717124, complete sequence.
AC058803
ACCESSION AC058803
VERSION AC058803.5 GI:17488731
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 203493)
Britten B., Linton L., Nussbaum C. and Lander E.
TITLE Homo sapiens chromosome 15, clone RP11-717124
JOURNAL Unpublished

QY 381 CCGGACTCAACATGCGCTGCTCGCCGGAGAGCGCTGCGCTGCGCGCGCTCGCTC 440
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Db 61 CCGGACTCAACATGCGCTGCTCGCCGGAGAGCGCTGCGCTGCGCGCTCGCTC 120
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QY 441 CTGCACG 447
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Db 121 CTGCACG 127

RESULT 6
US-08-660-451A-11
Sequence 11, Application US/08660451A
Parent No. 6524789

GENERAL INFORMATION:
APPLICANT: Elliott, Kathryn J.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA

COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,722
FILING DATE: 06/07/95

ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:

LENGTH: 1876 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:

NAME/KEY: Coding Sequence
LOCATION: 73...1581
OTHER INFORMATION: alpha7 human neuronal nicotinic
OTHER INFORMATION: acetylcholine receptor
NAME/KEY: 5'UTR
LOCATION: 1...72
OTHER INFORMATION:
NAME/KEY: 3'UTR
LOCATION: 1582...1876
OTHER INFORMATION:
US-08-660-451A-11

Query Match 27.8%; Score 127; DB 4; Length 1876;
Best Local Similarity 100.0%; Pred. No. 1,1e-15;

Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGCCTGAGGCGGAGCGCCGGGCGGAGAGCGAGACGAGAGCGCGCGCTGCTGACGCT 60
|||||
QY 381 CCGGACTCAACATGCGCTGCTCGCCGGAGAGCGCTGCGCTGCGCGCGCTCGCTC 440
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Db 61 CCGGACTCAACATGCGCTGCTCGCCGGAGAGCGCTGCGCTGCGCGCGCTCGCTC 120
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QY 441 CTGCACG 447
|||||
Db 121 CTGCACG 127

RESULT 7
US-08-318-837-1/c
Sequence 1, Application US/0831837
Patent No. 5981277

GENERAL INFORMATION:
APPLICANT: FRANSSEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE,
APPLICANT: ANDRE; VAN HEVERSWYN, HUGO
TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACID
TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAPY
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK

COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,837
FILING DATE: 13-OCT-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 93/01022
FILING DATE: 28-APR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 92,401,231.3
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,663
REFERENCE/DOCKET NUMBER: 410,007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2150 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: Human
TISSUE TYPE: Spleen tissue from healthy human
FEATURE:

NAME/KEY: CDS
LOCATION: 1810..1982
FEATURE:
NAME/KEY: misc_feature
LOCATION: 543

Db 121 CTGCACG 127

; sequence 7, Application US/09217345
; Patent No. 6303753

GENERAL INFORMATION:
APPLICANT: E11104

APPLICANT: Ellis, Steven B.
APPLICANT: [REDACTED]

AFFILIANT: Harpold, Michael M.
TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND

TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Halper & McClain

STREET: 1660 U
CITY: San Diego

STATE: CA
COUNTRY: USA

ZIP: 92101
COMPUTER READABLE FORM.

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,596
FILING DATE: 07-JUN-2008

EXPIRATION DATE: 07-JUN-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US94/02447

FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 08/149,503
FILING DATE: 08 NOV 1993

FILED DATE: 08-NOV-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IIS 07/938 154

FILING DATE: 30-NOV-1992
 PRIOR APPLICATION DATA

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/504,455

FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33 779

REFERENCE/DOCKET NUMBER: 6362-995
TELECOMMUNICATIONS INTRODUCTION

TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs

TYPE: nucleic acid

SHAPEDNESS: both
TOPOLOGY: both

MOLECULE TYPE: cDNA ;
FEATURE:

NAME/KEY: CDS
LOCATION: 73-1581

OTHER INFORMATION: /product= "ALPH

TT-965-184-80

| | | |
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| Query Match | 27.8%; | Score 12 |
| Best Local Similarity | 100.0%; | Pred. N |

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1 GGCCGAGCGCAGGCCCGGGCAGAC

61 CCGGACTCAACATGCGCTGCTCGCCCGGAGGCGTTCGGCGGCGCGCGCTGCTC 120

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2003, 08:56:10 ; Search time 68 Seconds
(without alignments)
2966.354 Million cell updates/sec

Title: US-08-956-518A-94
Perfect score: 457
Sequence: 1 AGAAGCGAGAGAGAGTAG.....CTCCTGCGCGTAAGCCAC 457

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

1 number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 127 | 27.8 | 1876 | 2 US-08-700-636-7 | Sequence 7, Appl |
| 3 | 127 | 27.8 | 1876 | 3 US-08-467-574-7 | Sequence 7, Appl |
| 4 | 127 | 27.8 | 1876 | 4 US-09-217-345-7 | Sequence 7, Appl |
| 5 | 127 | 27.8 | 1876 | 4 US-08-487-536-11 | Sequence 11, Appl |
| 6 | 127 | 27.8 | 1876 | 4 US-08-660-451A-11 | Sequence 11, Appl |
| 7 | 69.2 | 15.0 | 2150 | 2 US-08-318-837-1 | Sequence 16, Appl |
| 8 | 64 | 14.0 | 152331 | 3 US-09-128-155-16 | Sequence 13, Appl |
| 9 | 60.6 | 13.3 | 320 | 3 US-09-165-264-13 | Sequence 8, Appl |
| 10 | 60.2 | 13.2 | 319 | 3 US-09-165-264-8 | Sequence 7, Appl |
| 11 | 58.8 | 12.9 | 320 | 3 US-09-165-264-7 | Sequence 14, Appl |
| 12 | 58.8 | 12.9 | 320 | 3 US-09-165-264-14 | Sequence 11, Appl |
| 13 | 56.8 | 12.4 | 320 | 3 US-09-165-264-11 | Sequence 12, Appl |
| 14 | 56.4 | 12.3 | 318 | 3 US-09-165-264-12 | Sequence 11, Appl |
| 15 | 56.4 | 12.3 | 12001 | 1 US-08-458-568A-11 | Sequence 1, Appl |
| 16 | 56 | 12.3 | 1120 | 3 US-09-030-613-1 | Sequence 1, Appl |
| 17 | 56 | 12.3 | 1120 | 3 US-09-451-905-1 | Sequence 2, Appl |
| 18 | 54.8 | 12.0 | 4403765 | 3 US-09-103-840A-2 | Sequence 1, Appl |
| 19 | 54.2 | 11.9 | 23187 | 4 US-09-499-522-1 | Sequence 180, App |
| 20 | 54 | 11.8 | 2000 | 4 US-09-338-907-180 | Sequence 180, App |
| 21 | 54 | 11.8 | 2000 | 4 US-09-218-207-180 | Sequence 1, Appl |
| 22 | 54 | 11.8 | 56516 | 2 US-08-996-306-1 | Sequence 1, Appl |
| 23 | 54 | 11.8 | 56516 | 3 US-09-338-907-1 | Sequence 1, Appl |
| 24 | 54 | 11.8 | 56516 | 4 US-09-218-207-1 | Sequence 1, Appl |
| 25 | 54 | 11.8 | 56520 | 4 US-09-338-907-179 | Sequence 179, App |
| 26 | 54 | 11.8 | 56520 | 4 US-09-218-207-179 | Sequence 179, App |
| 27 | 53.2 | 11.6 | 4411529 | 3 US-09-103-840A-1 | Sequence 1, Appl |

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| C 28 | 53 | 11.6 | 4257 | 2 US-08-690-473-1 | Sequence 1, Appl |
| C 29 | 53 | 11.6 | 4257 | 3 US-09-259-821A-1 | Sequence 1, Appl |
| C 30 | 53 | 11.6 | 4257 | 3 US-08-843-659-1 | Sequence 1, Appl |
| C 31 | 53 | 11.6 | 12001 | 1 US-08-458-568A-11 | Sequence 3, Appl |
| C 32 | 52.4 | 11.5 | 5228 | 4 US-09-428-711A-15 | Sequence 15, Appl |
| C 33 | 52.4 | 11.5 | 5228 | 4 US-08-232-463-14 | Sequence 14, Appl |
| C 34 | 52.4 | 11.5 | 7218 | 1 US-08-232-463-14 | Sequence 2, Appl |
| C 35 | 52.4 | 11.5 | 4403765 | 3 US-09-103-840A-2 | Sequence 1, Appl |
| C 36 | 51.8 | 11.3 | 4403 | 2 US-08-284-941-1 | Sequence 1, Appl |
| C 37 | 51.8 | 11.3 | 4403 | 2 US-08-447-642-1 | Sequence 1, Appl |
| C 38 | 51.8 | 11.3 | 4403 | 3 US-09-236-503-1 | Sequence 1, Appl |
| C 39 | 51.8 | 11.3 | 4403 | 5 PCT-US93-02147A-1 | Sequence 1, Appl |
| C 40 | 51.8 | 11.3 | 4411529 | 3 US-09-103-840A-1 | Sequence 1, Appl |
| C 41 | 51.4 | 11.2 | 4060 | 1 US-08-308-949A-1 | Sequence 173, App |
| C 42 | 50.8 | 11.1 | 407 | 4 US-09-056-556-173 | Sequence 168, App |
| C 43 | 50.8 | 11.1 | 407 | 4 US-09-072-596-168 | Sequence 37, Appl |
| C 44 | 50.4 | 11.0 | 1292 | 3 US-08-483-533-37 | Sequence 37, Appl |
| C 45 | 50.4 | 11.0 | 1292 | 4 US-09-283-471A-37 | Sequence 37, Appl |

ALIGNMENTS

RESULT 1
US-08-466-589-7

; Sequence 7, Application US/08466589
; Patent No. 5837489

; GENERAL INFORMATION:

; APPLICANT: Eliot, Kathryn J.

; APPLICANT: Ellis, Steven B.

; APPLICANT: Harpold, Michael M.

; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE

; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ Version 1.5

; CURRENT APPLICATION DATA: